



- 1 -

SEQUENCE LISTING

<110> Bennett, Robert P.
Welch, Peter J.
Harwood, Steven
Madden, Knut
Frimpong, Kenneth
Franke, Kenneth E.

<120> Viral Vectors Containing Recombination Sites

<130> 0942.5450007

<140> US 10/622,088

<141> 2003-07-18

<150> PCT/US03/22437

<151> 2003-07-18

<150> US 60/396,335

<151> 2002-07-18

<150> US 60/398,617

<151> 2002-07-26

<150> US 60/427,231

<151> 2002-11-19

<150> US 60/456,496

<151> 2003-03-24

<150> US 60/474,940

<151> 2003-06-03

<160> 164

<170> PatentIn version 3.2

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<400> 45
taatacgact cactataggg 20

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<400> 46
accgaggaga gggtagggga t 21

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accgaggaga gggtaggga t 21

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| cgtggatagc | ggtttgactc | acggggattt | ccaagtctcc | accccatga | cgtcaatggg | 1200 |
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| ctaactagag | aaccctactgc | ttactggctt | atcgaaatta | atacgactca | ctatagggag | 1380 |
| acccaagctg | gctagttaag | ctatcaacaa | gtttgtacaa | aaaagctgaa | cgagaaacgt | 1440 |
| aaaatgatat | aaatatcaat | atattaaatt | agatttttgc | taaaaaacag | actacataat | 1500 |
| actgtaaaac | acaacatata | cagtcactat | gaatcaacta | cttagatggg | attagtgacc | 1560 |
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| tctggatttt | cagcctctat | acttactaaa | cgtgataaag | tttctgtaat | ttctactgta | 1920 |
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| gttaatggcg | tttttgatgt | catttttcgcg | gtggctgaga | tcagccactt | cttccccgat | 2040 |
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| ggattggctg | agacgaaaaa | catattctca | ataaaccttt | tagggaaata | ggccaggttt | 2880 |
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| gcattcatca | ggcgggcaag | aatgtgaata | aaggccggat | aaaacttgtg | cttatttttc | 3120 |
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<213> Unknown

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<220>
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```

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<212> DNA
<213> Artificial Sequence
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| | | | | | | |
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| | | | | 1 | | |
| att acg gat tca ctg gcc gtc gtt tta caa cgt | cgt gac tgg gaa aac | 2444 | | | | |
| Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg | Arg Asp Trp Glu Asn | | | | | |
| 5 | 10 | 15 | | | | |

| | |
|---|------|
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| agc tgg cgt aat agc gaa gag gcc cgc acc gat cgc cct tcc caa cag Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln 40 45 50 | 2540 |
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| gaa gcg gtg ccg gaa agc tgg ctg gag tgc gat ctt cct gag gcc gat Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro Glu Ala Asp 70 75 80 | 2636 |
| act gtc gtc gtc ccc tca aac tgg cag atg cac ggt tac gat gcg ccc Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr Asp Ala Pro 85 90 95 | 2684 |
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| gaa agc tgg cta cag gaa ggc cag acg cga att att ttt gat ggc gtt Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe Asp Gly Val 135 140 145 | 2828 |
| aac tcg gcg ttt cat ctg tgg tgc aac ggg cgc tgg gtc ggt tac ggc Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val Gly Tyr Gly 150 155 160 | 2876 |
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| gcc gga gaa aac cgc ctc gcg gtg atg gtg ctg cgt tgg agt gac ggc Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp Ser Asp Gly 180 185 190 195 | 2972 |
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| gtt gcc act cgc ttt aat gat gat ttc agc cgc gct gta ctg gag gct Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val Leu Glu Ala 230 235 240 | 3116 |
| gaa gtt cag atg tgc ggc gag ttg cgt gac tac cta cgg gta aca gtt Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg Val Thr Val 245 250 255 | 3164 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| tct | tta | tgg | cag | ggt | gaa | acg | cag | gtc | gcc | agc | ggc | acc | gcg | cct | ttc | 3212 |
| Ser | Leu | Trp | Gln | Gly | Glu | Thr | Gln | Val | Ala | Ser | Gly | Thr | Ala | Pro | Phe | |
| 260 | | | | | 265 | | | | | 270 | | | | | 275 | |
| ggc | ggt | gaa | att | atc | gat | gag | cgt | ggg | ggg | tat | gcc | gat | cgc | gtc | aca | 3260 |
| Gly | Gly | Glu | Ile | Ile | Asp | Glu | Arg | Gly | Gly | Tyr | Ala | Asp | Arg | Val | Thr | |
| | | | | 280 | | | | | 285 | | | | | | 290 | |
| cta | cgt | ctg | aac | gtc | gaa | aac | ccg | aaa | ctg | tgg | agc | gcc | gaa | atc | ccg | 3308 |
| Leu | Arg | Leu | Asn | Val | Glu | Asn | Pro | Lys | Leu | Trp | Ser | Ala | Glu | Ile | Pro | |
| | | | 295 | | | | | 300 | | | | | 305 | | | |
| aat | ctc | tat | cgt | gcg | gtg | gtt | gaa | ctg | cac | acc | gcc | gac | ggc | acg | ctg | 3356 |
| Asn | Leu | Tyr | Arg | Ala | Val | Val | Glu | Leu | His | Thr | Ala | Asp | Gly | Thr | Leu | |
| | | 310 | | | | | 315 | | | | | 320 | | | | |
| att | gaa | gca | gaa | gcc | tgc | gat | gtc | ggg | ttc | cgc | gag | gtg | cgg | att | gaa | 3404 |
| Ile | Glu | Ala | Glu | Ala | Cys | Asp | Val | Gly | Phe | Arg | Glu | Val | Arg | Ile | Glu | |
| | 325 | | | | | 330 | | | | | 335 | | | | | |
| aat | ggg | ctg | ctg | ctg | ctg | aac | ggc | aag | ccg | ttg | ctg | att | cga | ggc | gtt | 3452 |
| Asn | Gly | Leu | Leu | Leu | Leu | Asn | Gly | Lys | Pro | Leu | Leu | Ile | Arg | Gly | Val | |
| 340 | | | | | 345 | | | | | 350 | | | | | 355 | |
| aac | cgt | cac | gag | cat | cat | cct | ctg | cat | ggg | cag | gtc | atg | gat | gag | cag | 3500 |
| Asn | Arg | His | Glu | His | His | Pro | Leu | His | Gly | Gln | Val | Met | Asp | Glu | Gln | |
| | | | | 360 | | | | | 365 | | | | | 370 | | |
| acg | atg | gtg | cag | gat | atc | ctg | ctg | atg | aag | cag | aac | aac | ttt | aac | gcc | 3548 |
| Thr | Met | Val | Gln | Asp | Ile | Leu | Leu | Met | Lys | Gln | Asn | Asn | Phe | Asn | Ala | |
| | | | 375 | | | | | 380 | | | | | 385 | | | |
| gtg | cgc | tgt | tcg | cat | tat | ccg | aac | cat | ccg | ctg | tgg | tac | acg | ctg | tgc | 3596 |
| Val | Arg | Cys | Ser | His | Tyr | Pro | Asn | His | Pro | Leu | Trp | Tyr | Thr | Leu | Cys | |
| | | 390 | | | | | 395 | | | | | 400 | | | | |
| gac | cgc | tac | ggc | ctg | tat | gtg | gtg | gat | gaa | gcc | aat | att | gaa | acc | cac | 3644 |
| Asp | Arg | Tyr | Gly | Leu | Tyr | Val | Val | Asp | Glu | Ala | Asn | Ile | Glu | Thr | His | |
| | 405 | | | | | 410 | | | | | 415 | | | | | |
| ggc | atg | gtg | cca | atg | aat | cgt | ctg | acc | gat | gat | ccg | cgc | tgg | cta | ccg | 3692 |
| Gly | Met | Val | Pro | Met | Asn | Arg | Leu | Thr | Asp | Asp | Pro | Arg | Trp | Leu | Pro | |
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| gcg | atg | agc | gaa | cgc | gta | acg | cga | atg | gtg | cag | cgc | gat | cgt | aat | cac | 3740 |
| Ala | Met | Ser | Glu | Arg | Val | Thr | Arg | Met | Val | Gln | Arg | Asp | Arg | Asn | His | |
| | | | | 440 | | | | | 445 | | | | | 450 | | |
| ccg | agt | gtg | atc | atc | tgg | tcg | ctg | ggg | aat | gaa | tca | ggc | cac | ggc | gct | 3788 |
| Pro | Ser | Val | Ile | Ile | Trp | Ser | Leu | Gly | Asn | Glu | Ser | Gly | His | Gly | Ala | |
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| aat | cac | gac | gcg | ctg | tat | cgc | tgg | atc | aaa | tct | gtc | gat | cct | tcc | cgc | 3836 |
| Asn | His | Asp | Ala | Leu | Tyr | Arg | Trp | Ile | Lys | Ser | Val | Asp | Pro | Ser | Arg | |
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| ccg | gtg | cag | tat | gaa | ggc | ggc | gga | gcc | gac | acc | acg | gcc | acc | gat | att | 3884 |
| Pro | Val | Gln | Tyr | Glu | Gly | Gly | Gly | Ala | Asp | Thr | | Thr | Ala | Thr | Ile | |
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| | | | | | | | | | | | | | | | | |
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| Ile 500 | Cys | Pro | Met | Tyr | Ala 505 | Arg | Val | Asp | Glu | Asp 510 | Gln | Pro | Phe | Pro | Ala 515 | |
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| Val | Pro | Lys | Trp | Ser | Ile | Lys | Lys | Trp | Leu | Ser | Leu | Pro | Gly | Glu | Thr | |
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| cgc | ccg | ctg | atc | ctt | tgc | gaa | tac | gcc | cac | gcg | atg | ggt | aac | agt | ctt | 4028 |
| Arg | Pro | Leu | Ile | Leu | Cys | Glu | Tyr | Ala | His | Ala | Met | Gly | Asn | Ser | Leu | |
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| ggc | ggt | ttc | gct | aaa | tac | tgg | cag | gcg | ttt | cgt | cag | tat | ccc | cgt | tta | 4076 |
| Gly | Gly | Phe | Ala | Lys | Tyr | Trp | Gln | Ala | Phe | Arg | Gln | Tyr | Pro | Arg | Leu | |
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| cag | ggc | ggc | ttc | gtc | tgg | gac | tgg | gtg | gat | cag | tcg | ctg | att | aaa | tat | 4124 |
| Gln | Gly | Gly | Phe | Val | Trp | Asp | Trp | Val | Asp | Gln | Ser | Leu | Ile | Lys | Tyr | |
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| gat | gaa | aac | ggc | aac | ccg | tgg | tcg | gct | tac | ggc | ggt | gat | ttt | ggc | gat | 4172 |
| Asp | Glu | Asn | Gly | Asn | Pro | Trp | Ser | Ala | Tyr | Gly | Gly | Asp | Phe | Gly | Asp | |
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| acg | ccg | aac | gat | cgc | cag | ttc | tgt | atg | aac | ggt | ctg | gtc | ttt | gcc | gac | 4220 |
| Thr | Pro | Asn | Asp | Arg | Gln | Phe | Cys | Met | Asn | Gly | Leu | Val | Phe | Ala | Asp | |
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| cgc | acg | ccg | cat | cca | gcg | ctg | acg | gaa | gca | aaa | cac | cag | cag | cag | ttt | 4268 |
| Arg | Thr | Pro | His | Pro | Ala | Leu | Thr | Glu | Ala | Lys | His | Gln | Gln | Gln | Phe | |
| | | | 615 | | | | | 620 | | | | | 625 | | | |
| ttc | cag | ttc | cgt | tta | tcc | ggg | caa | acc | atc | gaa | gtg | acc | agc | gaa | tac | 4316 |
| Phe | Gln | Phe | Arg | Leu | Ser | Gly | Gln | Thr | Ile | Glu | Val | Thr | Ser | Glu | Tyr | |
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| ctg | ttc | cgt | cat | agc | gat | aac | gag | ctc | ctg | cac | tgg | atg | gtg | gcg | ctg | 4364 |
| Leu | Phe | Arg | His | Ser | Asp | Asn | Glu | Leu | Leu | His | Trp | Met | Val | Ala | Leu | |
| | 645 | | | | | 650 | | | | | 655 | | | | | |
| gat | ggt | aag | ccg | ctg | gca | agc | ggt | gaa | gtg | cct | ctg | gat | gtc | gct | cca | 4412 |
| Asp | Gly | Lys | Pro | Leu | Ala | Ser | Gly | Glu | Val | Pro | Leu | Asp | Val | Ala | Pro | |
| 660 | | | | | 665 | | | | | 670 | | | | | 675 | |
| caa | ggt | aaa | cag | ttg | att | gaa | ctg | cct | gaa | cta | ccg | cag | ccg | gag | agc | 4460 |
| Gln | Gly | Lys | Gln | Leu | Ile | Glu | Leu | Pro | Glu | Leu | Pro | Gln | Pro | Glu | Ser | |
| | | | | 680 | | | | | 685 | | | | | 690 | | |
| gcc | ggg | caa | ctc | tgg | ctc | aca | gta | cgc | gta | gtg | caa | ccg | aac | gcg | acc | 4508 |
| Ala | Gly | Gln | Leu | Trp | Leu | Thr | Val | Arg | Val | Val | Gln | Pro | Asn | Ala | Thr | |
| | | | 695 | | | | | 700 | | | | | 705 | | | |
| gca | tgg | tca | gaa | gcc | ggg | cac | atc | agc | gcc | tgg | cag | cag | tgg | cgt | ctg | 4556 |
| Ala | Trp | Ser | Glu | Ala | Gly | His | Ile | Ser | Ala | Trp | Gln | Gln | Trp | Arg | Leu | |
| | | 710 | | | | | 715 | | | | | | 720 | | | |
| gcg | gaa | aac | ctc | agt | gtg | acg | ctc | ccc | gcc | gcg | tcc | cac | gcc | atc | ccg | 4604 |
| Ala | Glu | Asn | Leu | Ser | Val | Thr | Leu | Pro | Ala | Ala | Ser | His | Ala | Ile | Pro | |
| | 725 | | | | | | 730 | | | | 735 | | | | | |
| cat | ctg | acc | acc | agc | gaa | atg | gat | ttt | tgc | atc | gag | ctg | ggt | aat | aag | 4652 |
| His | Leu | Thr | Thr | Ser | Glu | Met | Asp | Phe | Cys | Ile | Glu | Leu | Gly | Asn | Lys | |

| 740 | | | | 745 | | | | 750 | | | | 755 | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| cgt | tgg | caa | ttt | aac | cgc | cag | tca | ggc | ttt | ctt | tca | cag | atg | tgg | att | 4700 |
| Arg | Trp | Gln | Phe | Asn | Arg | Gln | Ser | Gly | Phe | Leu | Ser | Gln | Met | Trp | Ile | |
| 760 | | | | 765 | | | | 770 | | | | | | | | |
| ggc | gat | aaa | aaa | caa | ctg | ctg | acg | ccg | ctg | cgc | gat | cag | ttc | acc | cgt | 4748 |
| Gly | Asp | Lys | Lys | Gln | Leu | Leu | Thr | Pro | Leu | Arg | Asp | Gln | Phe | Thr | Arg | |
| 775 | | | | 780 | | | | 785 | | | | | | | | |
| gca | ccg | ctg | gat | aac | gac | att | ggc | gta | agt | gaa | gcg | acc | cgc | att | gac | 4796 |
| Ala | Pro | Leu | Asp | Asn | Asp | Ile | Gly | Val | Ser | Glu | Ala | Thr | Arg | Ile | Asp | |
| 790 | | | | 795 | | | | 800 | | | | | | | | |
| cct | aac | gcc | tgg | gtc | gaa | cgc | tgg | aag | gcg | gcg | ggc | cat | tac | cag | gcc | 4844 |
| Pro | Asn | Ala | Trp | Val | Glu | Arg | Trp | Lys | Ala | Ala | Gly | His | Tyr | Gln | Ala | |
| 805 | | | | 810 | | | | 815 | | | | | | | | |
| gaa | gca | gcg | ttg | ttg | cag | tgc | acg | gca | gat | aca | ctt | gct | gat | gcg | gtg | 4892 |
| Glu | Ala | Ala | Leu | Leu | Gln | Cys | Thr | Ala | Asp | Thr | Leu | Ala | Asp | Ala | Val | |
| 820 | | | | 825 | | | | 830 | | | | 835 | | | | |
| ctg | att | acg | acc | gct | cac | gcg | tgg | cag | cat | cag | ggg | aaa | acc | tta | ttt | 4940 |
| Leu | Ile | Thr | Thr | Ala | His | Ala | Trp | Gln | His | Gln | Gly | Lys | Thr | Leu | Phe | |
| 840 | | | | 845 | | | | 850 | | | | | | | | |
| atc | agc | cgg | aaa | acc | tac | cgg | att | gat | ggg | agt | ggg | caa | atg | gcg | att | 4988 |
| Ile | Ser | Arg | Lys | Thr | Tyr | Arg | Ile | Asp | Gly | Ser | Gly | Gln | Met | Ala | Ile | |
| 855 | | | | 860 | | | | 865 | | | | | | | | |
| acc | gtt | gat | gtt | gaa | gtg | gcg | agc | gat | aca | ccg | cat | ccg | gcg | cgg | att | 5036 |
| Thr | Val | Asp | Val | Glu | Val | Ala | Ser | Asp | Thr | Pro | His | Pro | Ala | Arg | Ile | |
| 870 | | | | 875 | | | | 880 | | | | | | | | |
| ggc | ctg | aac | tgc | cag | ctg | gcg | cag | gta | gca | gag | ccg | gta | aac | tgg | ctc | 5084 |
| Gly | Leu | Asn | Cys | Gln | Leu | Ala | Gln | Val | Ala | Glu | Arg | Val | Asn | Trp | Leu | |
| 885 | | | | 890 | | | | 895 | | | | | | | | |
| gga | tta | ggg | ccg | caa | gaa | aac | tat | ccc | gac | cgc | ctt | act | gcc | gcc | tgt | 5132 |
| Gly | Leu | Gly | Pro | Gln | Glu | Asn | Tyr | Pro | Asp | Arg | Leu | Thr | Ala | Ala | Cys | |
| 900 | | | | 905 | | | | 910 | | | | 915 | | | | |
| ttt | gac | cgc | tgg | gat | ctg | cca | ttg | tca | gac | atg | tat | acc | ccg | tac | gtc | 5180 |
| Phe | Asp | Arg | Trp | Asp | Leu | Pro | Leu | Ser | Asp | Met | Tyr | Thr | Pro | Tyr | Val | |
| 920 | | | | 925 | | | | 930 | | | | | | | | |
| ttc | ccg | agc | gaa | aac | ggt | ctg | cgc | tgc | ggg | acg | cgc | gaa | ttg | aat | tat | 5228 |
| Phe | Pro | Ser | Glu | Asn | Gly | Leu | Arg | Cys | Gly | Thr | Arg | Glu | Leu | Asn | Tyr | |
| 935 | | | | 940 | | | | 945 | | | | | | | | |
| ggc | cca | cac | cag | tgg | cgc | ggc | gac | ttc | cag | ttc | aac | atc | agc | cgc | tac | 5276 |
| Gly | Pro | His | Gln | Trp | Arg | Gly | Asp | Phe | Gln | Phe | Asn | Ile | Ser | Arg | Tyr | |
| 950 | | | | 955 | | | | 960 | | | | | | | | |
| agt | caa | cag | caa | ctg | atg | gaa | acc | agc | cat | cgc | cat | ctg | ctg | cac | gcg | 5324 |
| Ser | Gln | Gln | Gln | Leu | Met | Glu | Thr | Ser | His | Arg | His | Leu | Leu | His | Ala | |
| 965 | | | | 970 | | | | 975 | | | | | | | | |
| gaa | gaa | ggc | aca | tgg | ctg | aat | atc | gac | ggt | ttc | cat | atg | ggg | att | ggt | 5372 |
| Glu | Glu | Gly | Thr | Trp | Leu | Asn | Ile | Asp | Gly | Phe | His | Met | Gly | Ile | Gly | |
| 980 | | | | 985 | | | | 990 | | | | 995 | | | | |

ggc gac gac tcc tgg agc ccg tca gta tcg gcg gaa ttc cag ctg 5417
 Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe Gln Leu
 1000 1005 1010

agc gcc ggt cgc tac cat tac cag ttg gtc tgg tgt caa aaa taa 5462
 Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln Lys
 1015 1020

tgactgcagg tcgaccatag tgactggata tgttgtgttt tacagtatta tgtagtctgt 5522

tttttatgca aaatctaatt taatatattg atatttatat cattttacgt ttctcgttca 5582

gctttcttgt acaaagtggg gagaatgaat gaagatctg ggg aag cct atc cct 5636
 Gly Lys Pro Ile Pro
 1025

aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt cat cat cac 5681
 Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His
 1030 1035 1040

cat cac cat tga 5693
 His His His
 1045

<210> 91
 <211> 1024
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> V5-His DEST cassette

<400> 91

Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu Gln Arg Arg Asp
 1 5 10 15

Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
 20 25 30

Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
 35 40 45

Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
 50 55 60

Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro
 65 70 75 80

Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
 85 90 95

Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro

| 100 | | | | | 105 | | | | | 110 | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Phe | Val | Pro | Thr | Glu | Asn | Pro | Thr | Gly | Cys | Tyr | Ser | Leu | Thr | Phe | |
| 115 | | | | | 120 | | | | | 125 | | | | | | |
| Asn | Val | Asp | Glu | Ser | Trp | Leu | Gln | Glu | Gly | Gln | Thr | Arg | Ile | Ile | Phe | |
| 130 | | | | | 135 | | | | | 140 | | | | | | |
| Asp | Gly | Val | Asn | Ser | Ala | Phe | His | Leu | Trp | Cys | Asn | Gly | Arg | Trp | Val | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Gly | Tyr | Gly | Gln | Asp | Ser | Arg | Leu | Pro | Ser | Glu | Phe | Asp | Leu | Ser | Ala | |
| 165 | | | | | 170 | | | | | 175 | | | | | | |
| Phe | Leu | Arg | Ala | Gly | Glu | Asn | Arg | Leu | Ala | Val | Met | Val | Leu | Arg | Trp | |
| 180 | | | | | 185 | | | | | 190 | | | | | | |
| Ser | Asp | Gly | Ser | Tyr | Leu | Glu | Asp | Gln | Asp | Met | Trp | Arg | Met | Ser | Gly | |
| 195 | | | | | 200 | | | | | 205 | | | | | | |
| Ile | Phe | Arg | Asp | Val | Ser | Leu | Leu | His | Lys | Pro | Thr | Thr | Gln | Ile | Ser | |
| 210 | | | | | 215 | | | | | 220 | | | | | | |
| Asp | Phe | His | Val | Ala | Thr | Arg | Phe | Asn | Asp | Asp | Phe | Ser | Arg | Ala | Val | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Glu | Ala | Glu | Val | Gln | Met | Cys | Gly | Glu | Leu | Arg | Asp | Tyr | Leu | Arg | |
| 245 | | | | | 250 | | | | | 255 | | | | | | |
| Val | Thr | Val | Ser | Leu | Trp | Gln | Gly | Glu | Thr | Gln | Val | Ala | Ser | Gly | Thr | |
| 260 | | | | | 265 | | | | | 270 | | | | | | |
| Ala | Pro | Phe | Gly | Gly | Glu | Ile | Ile | Asp | Glu | Arg | Gly | Gly | Tyr | Ala | Asp | |
| 275 | | | | | 280 | | | | | 285 | | | | | | |
| Arg | Val | Thr | Leu | Arg | Leu | Asn | Val | Glu | Asn | Pro | Lys | Leu | Trp | Ser | Ala | |
| 290 | | | | | 295 | | | | | 300 | | | | | | |
| Glu | Ile | Pro | Asn | Leu | Tyr | Arg | Ala | Val | Val | Glu | Leu | His | Thr | Ala | Asp | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Gly | Thr | Leu | Ile | Glu | Ala | Glu | Ala | Cys | Asp | Val | Gly | Phe | Arg | Glu | Val | |
| 325 | | | | | 330 | | | | | 335 | | | | | | |
| Arg | Ile | Glu | Asn | Gly | Leu | Leu | Leu | Leu | Asn | Gly | Lys | Pro | Leu | Leu | Ile | |
| 340 | | | | | 345 | | | | | 350 | | | | | | |

Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met
355 360 365

Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn
370 375 380

Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr
385 390 395 400

Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile
405 410 415

Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg
420 425 430

Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp
435 440 445

Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly
450 455 460

His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp
465 470 475 480

Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly Ala Asp Thr Thr Ala
485 490 495

Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro
500 505 510

Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro
515 520 525

Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly
530 535 540

Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr
545 550 555 560

Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu
565 570 575

Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp
580 585 590

Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val
595 600 605

Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln
610 615 620

Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr
625 630 635 640

Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met
645 650 655

Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp
660 665 670

Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gln
675 680 685

Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro
690 695 700

Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln
705 710 715 720

Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro Ala Ala Ser His
725 730 735

Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe Cys Ile Glu Leu
740 745 750

Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln
755 760 765

Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln
770 775 780

Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr
785 790 795 800

Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His
805 810 815

Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala
820 825 830

Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln His Gln Gly Lys
835 840 845

Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln
850 855 860

Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro
865 870 875 880

Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val Ala Glu Arg Val
885 890 895

Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr
900 905 910

Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr
915 920 925

Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu
930 935 940

Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile
945 950 955 960

Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu
965 970 975

Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met
980 985 990

Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe
995 1000 1005

Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln
1010 1015 1020

Lys

<210> 92
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> V5-His DEST cassette

<400> 92

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
1 5 10 15

Gly His His His His His His
20

<210> 93
<211> 376
<212> PRT
<213> Herpesvirus sp.

<400> 93

Met Ala Ser Tyr Pro Cys His Gln His Ala Ser Ala Phe Asp Gln Ala
1 5 10 15

Ala Arg Ser Arg Gly His Asn Asn Arg Arg Thr Ala Leu Arg Pro Arg
20 25 30

Arg Gln Gln Lys Ala Thr Glu Val Arg Leu Glu Gln Lys Met Pro Thr
35 40 45

Leu Leu Arg Val Tyr Ile Asp Gly Pro His Gly Met Gly Lys Thr Thr
50 55 60

Thr Thr Gln Leu Leu Val Ala Leu Gly Ser Arg Asp Asp Ile Val Tyr
65 70 75 80

Val Pro Glu Pro Met Thr Tyr Trp Arg Val Leu Gly Ala Ser Glu Thr
85 90 95

Ile Ala Asn Ile Tyr Thr Thr Gln His Arg Leu Asp Gln Gly Glu Ile
100 105 110

Ser Ala Gly Asp Ala Ala Val Val Met Thr Ser Ala Gln Ile Thr Met
115 120 125

Gly Met Pro Tyr Ala Val Thr Asp Ala Val Leu Ala Pro His Ile Gly
130 135 140

Gly Glu Ala Gly Ser Ser His Ala Pro Pro Pro Ala Leu Thr Leu Ile
145 150 155 160

Phe Asp Arg His Pro Ile Ala Ala Leu Leu Cys Tyr Pro Ala Ala Arg
165 170 175

Tyr Leu Met Gly Ser Met Thr Pro Gln Ala Val Leu Ala Phe Val Ala

| 180 | | | | | 185 | | | | | 190 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Pro | Pro | Thr | Leu | Pro | Gly | Thr | Asn | Ile | Val | Leu | Gly | Ala | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Glu | Asp | Arg | His | Ile | Asp | Arg | Leu | Ala | Lys | Arg | Gln | Arg | Pro | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Glu | Arg | Leu | Asp | Leu | Ala | Met | Leu | Ala | Ala | Ile | Arg | Arg | Val | Tyr | Gly |
| 225 | | | | | | 230 | | | | | 235 | | | | 240 |
| Leu | Leu | Ala | Asn | Thr | Val | Arg | Tyr | Leu | Gln | Gly | Gly | Gly | Ser | Trp | Arg |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Glu | Asp | Trp | Gly | Gln | Leu | Ser | Gly | Ala | Ala | Val | Pro | Pro | Gln | Gly | Ala |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Glu | Pro | Gln | Ser | Asn | Ala | Gly | Pro | Arg | Pro | His | Ile | Gly | Asp | Thr | Leu |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Phe | Thr | Leu | Phe | Arg | Ala | Pro | Glu | Leu | Leu | Ala | Pro | Asn | Gly | Asp | Leu |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Tyr | Asn | Val | Phe | Ala | Trp | Ala | Leu | Asp | Val | Leu | Ala | Lys | Arg | Leu | Arg |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 |
| Pro | Met | His | Val | Phe | Ile | Leu | Asp | Tyr | Asp | Gln | Ser | Pro | Ala | Gly | Cys |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Arg | Asp | Ala | Leu | Leu | Gln | Leu | Thr | Ser | Gly | Met | Val | Gln | Thr | His | Val |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Thr | Thr | Pro | Gly | Ser | Ile | Pro | Thr | Ile | Cys | Asp | Leu | Ala | Arg | Thr | Phe |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Ala | Arg | Glu | Met | Gly | Glu | Ala | Asn | | | | | | | | |
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<210> 94
 <211> 5763
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Mel/V5-His DEST cassette

 <220>

<221> CDS
<222> (102) .. (164)

<220>
<221> gene
<222> (591) .. (1770)

<220>
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<222> (5692) .. (5763)

<400> 94
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ttattcatac cgtcccacca tcgggcgcgg atcctataaa t atg aaa ttc tta gtc 116
Met Lys Phe Leu Val
1 5

aac gtt gcc ctt gtt ttt atg gtc gta tac att tct tac atc tat gcg 164
Asn Val Ala Leu Val Phe Met Val Val Tyr Ile Ser Tyr Ile Tyr Ala
10 15 20

gcatggtcga atcaaacaag tttgtacaaa aaagctgaac gagaaacgta aaatgatata 224

aatatcaata tattaaatta gat ttttgc at aaaaaacaga ctacataata ctgtaaaaca 284

caacatatcc agtcactatg gcggccgctc cctaaccac ggggcccgtg gctatggcag 344

ggcttgccgc cccgacgttg gctgcgagcc ctgggccttc acccgaactt gggggttggg 404

gtggggaaaa ggaagaaacg cgggcgtatt ggtcccaatg ggggtctcggg ggggtatcga 464

cagagtgcc a gccctgggac cgaaccccg gtttatgaac aaacgacca acaccgtgc 524

gtttttattct gtctttttat tgccgtcata gcgcgggttc cttccggtat tgtctccttc 584

cgtgtttcag ttagcctccc ccatctcccg ggcaaacgtg cgcgccaggc cgcagatcgt 644

cggatatggag cctgggggtg tgacgtgggt ctggaccatc ccggaggtaa gttgcagcag 704

ggcgtcccgg cagccggcgg gcgattgggc gtaatccagg ataaagacat gcatgggacg 764

gaggcgtttg gccaaagcgt ccaaagccca ggcaaacacg ttatacaggc cgcggttggg 824

ggccagcaac tcggggggccc gaaacagggt aaataacgtg tccccgatat ggggtcgtgg 884

gcccgcgttg ctctggggct cggcacccctg gggcggcacg gccgcccccg aaagctgtcc 944

ccaatcctcc cgccacgacc cgccgccttg cagataccgc accgtattgg caagcagccc 1004

ataaacgcgg cgaatcgcgg ccagcatagc cagggtcaagc cgctcgccgg ggcgctggcg 1064

tttggccagg cggtcgatgt gtctgtctc cggaagggcc cccaacacga tgtttgtgcc 1124

gggcaaggtc ggcgggatga gggccacgaa cgccagcacg gcctgggggg tcatgctgcc 1184

cataaggtat cgcgcggccg ggtagcacag gagggcggcg atgggatggc ggtcgaagat 1244

| | |
|--|------|
| gaggggtgagg gccgggggag gggcatgtga gctcccagcc tccccccga tatgaggagc | 1304 |
| cagaacggcg tcgggtcacgg cataaggcat gccattgtt atctgggagc ttgtcattac | 1364 |
| caccgcccgc tccccggccg atatctcacc ctgggtcagg cggtgttggtg tgggttagat | 1424 |
| gttcgagatt gtctcggaag cccccaacac ccgccagtaa gtcacaggct cgggtacgta | 1484 |
| gacgatatcg tcgcgcaaac ccagggccac cagcagttgc gtgggtgggtg ttttcccat | 1544 |
| cccgtgggga ccgtctatat aaaccgcag tagcgtgggc attttctgct ccaggcggac | 1604 |
| ttccgtggct ttttgttgcc ggcgagggcg caacgccgta cgtcggttgt tatggccgcg | 1664 |
| agaacgcgca gcctggtcga acgcagacgc gtgttgatgg caggggtacg aagccataga | 1724 |
| tcccgttatc aattacttat actatccggc gcgcaagcga gcgtgtgcgc cggagcacia | 1784 |
| ttgatactga tttacgagtt gggcaaacgg gctttatata gcctgtcccc tccacagccc | 1844 |
| tagtgccgtg cgcaaagtgc ctacgtgacc aggcctctct acgcatatac aatcttatct | 1904 |
| ctatagataa ggtttccata tataaagcct ctcgatggct gaacgtgcac agtatcgtgt | 1964 |
| tgattttctga gtgctaacta acagttacaa tgaaccgttt ttttcgagag aataacattt | 2024 |
| ttgacgcgcc aaggaccggg ggcaagggtc gtgccaaatc tttgccagcg cctgccgcca | 2084 |
| actcgcgcc gcgcctgtt cgtccgccgc caaaatctaa catcaaacca cctacgcgca | 2144 |
| tctctccgcc taaacagcct atgtgcacct ctccggccaa gccgttgag cacagcagca | 2204 |
| ttgtaagtaa aaaaccagtc gtcaacagaa aagatggata ttttggtccg cccgagtttg | 2264 |
| ggaacaagtt tgaagggttg ccgcgtaca gcgacaaact ggatttcaaa caagagcgcg | 2324 |
| atctacgtac ctgcaggccc gggctcaacc caacacaata tattatagtt aaataagaat | 2384 |
| tattatcaaa tcatttgtat attaattaaa atactatact gttaaattaca ttttatttac | 2444 |
| aattcactct aga atg acc atg att acg gat tca ctg gcc gtc gtt tta | 2493 |
| Met Thr Met Ile Thr Asp Ser Leu Ala Val Val Leu | |
| 25 30 | |
| caa cgt cgt gac tgg gaa aac cct ggc gtt acc caa ctt aat cgc ctt | 2541 |
| Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu | |
| 35 40 45 | |
| gca gca cat ccc cct ttc gcc agc tgg cgt aat agc gaa gag gcc cgc | 2589 |
| Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg | |
| 50 55 60 65 | |
| acc gat cgc cct tcc caa cag ttg cgc agc ctg aat ggc gaa tgg cgc | 2637 |
| Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg | |
| 70 75 80 | |
| ttt gcc tgg ttt ccg gca cca gaa gcg gtg ccg gaa agc tgg ctg gag | 2685 |
| Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu | |
| 85 90 95 | |

| | |
|---|------|
| tgc gat ctt cct gag gcc gat act gtc gtc gtc ccc tca aac tgg cag | 2733 |
| Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln | |
| 100 105 110 | |
| atg cac ggt tac gat gcg ccc atc tac acc aac gta acc tat ccc att | 2781 |
| Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile | |
| 115 120 125 | |
| acg gtc aat ccg ccg ttt gtt ccc acg gag aat ccg acg ggt tgt tac | 2829 |
| Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr | |
| 130 135 140 145 | |
| tcg ctc aca ttt aat gtt gat gaa agc tgg cta cag gaa ggc cag acg | 2877 |
| Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr | |
| 150 155 160 | |
| cga att att ttt gat ggc gtt aac tcg gcg ttt cat ctg tgg tgc aac | 2925 |
| Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn | |
| 165 170 175 | |
| ggg cgc tgg gtc ggt tac ggc cag gac agt cgt ttg ccg tct gaa ttt | 2973 |
| Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe | |
| 180 185 190 | |
| gac ctg agc gca ttt tta cgc gcc gga gaa aac cgc ctc gcg gtg atg | 3021 |
| Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met | |
| 195 200 205 | |
| gtg ctg cgt tgg agt gac ggc agt tat ctg gaa gat cag gat atg tgg | 3069 |
| Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp | |
| 210 215 220 225 | |
| cgg atg agc ggc att ttc cgt gac gtc tcg ttg ctg cat aaa ccg act | 3117 |
| Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr | |
| 230 235 240 | |
| aca caa atc agc gat ttc cat gtt gcc act cgc ttt aat gat gat ttc | 3165 |
| Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe | |
| 245 250 255 | |
| agc cgc gct gta ctg gag gct gaa gtt cag atg tgc ggc gag ttg cgt | 3213 |
| Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg | |
| 260 265 270 | |
| gac tac cta cgg gta aca gtt tct tta tgg cag ggt gaa acg cag gtc | 3261 |
| Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val | |
| 275 280 285 | |
| gcc agc ggc acc gcg cct ttc ggc ggt gaa att atc gat gag cgt ggt | 3309 |
| Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly | |
| 290 295 300 305 | |
| ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg aaa | 3357 |
| Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys | |
| 310 315 320 | |
| ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa ctg | 3405 |
| Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu | |
| 325 330 335 | |
| cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc ggt | 3453 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| His | Thr | Ala | Asp | Gly | Thr | Leu | Ile | Glu | Ala | Glu | Ala | Cys | Asp | Val | Gly | | |
| | | 340 | | | | | 345 | | | | | 350 | | | | | |
| ttc | cgc | gag | gtg | cgg | att | gaa | aat | ggc | ctg | ctg | ctg | ctg | aac | ggc | aag | 3501 | |
| Phe | Arg | Glu | Val | Arg | Ile | Glu | Asn | Gly | Leu | Leu | Leu | Leu | Asn | Gly | Lys | | |
| | 355 | | | | | 360 | | | | | 365 | | | | | | |
| ccg | ttg | ctg | att | cga | ggc | gtt | aac | cgt | cac | gag | cat | cat | cct | ctg | cat | 3549 | |
| Pro | Leu | Leu | Ile | Arg | Gly | Val | Asn | Arg | His | Glu | His | His | Pro | Leu | His | | |
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| ggc | cag | gtc | atg | gat | gag | cag | acg | atg | gtg | cag | gat | atc | ctg | ctg | atg | 3597 | |
| Gly | Gln | Val | Met | Asp | Glu | Gln | Thr | Met | Val | Gln | Asp | Ile | Leu | Leu | Met | | |
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| aag | cag | aac | aac | ttt | aac | gcc | gtg | cgc | tgt | tcg | cat | tat | ccg | aac | cat | 3645 | |
| Lys | Gln | Asn | Asn | Phe | Asn | Ala | Val | Arg | Cys | Ser | His | Tyr | Pro | Asn | His | | |
| | | | 405 | | | | | 410 | | | | | 415 | | | | |
| ccg | ctg | tgg | tac | acg | ctg | tgc | gac | cgc | tac | ggc | ctg | tat | gtg | gtg | gat | 3693 | |
| Pro | Leu | Trp | Tyr | Thr | Leu | Cys | Asp | Arg | Tyr | Gly | Leu | Tyr | Val | Val | Asp | | |
| | | 420 | | | | | 425 | | | | | 430 | | | | | |
| gaa | gcc | aat | att | gaa | acc | cac | ggc | atg | gtg | cca | atg | aat | cgt | ctg | acc | 3741 | |
| Glu | Ala | Asn | Ile | Glu | Thr | His | Gly | Met | Val | Pro | Met | Asn | Arg | Leu | Thr | | |
| | 435 | | | | | 440 | | | | | 445 | | | | | | |
| gat | gat | ccg | cgc | tgg | cta | ccg | gcg | atg | agc | gaa | cgc | gta | acg | cga | atg | 3789 | |
| Asp | Asp | Pro | Arg | Trp | Leu | Pro | Ala | Met | Ser | Glu | Arg | Val | Thr | Arg | Met | | |
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| gtg | cag | cgc | gat | cgt | aat | cac | ccg | agt | gtg | atc | atc | tgg | tcg | ctg | ggg | 3837 | |
| Val | Gln | Arg | Asp | Arg | Asn | His | Pro | Ser | Val | Ile | Ile | Trp | Ser | Leu | Gly | | |
| | | | | 470 | | | | | 475 | | | | | 480 | | | |
| aat | gaa | tca | ggc | cac | ggc | gct | aat | cac | gac | gcg | ctg | tat | cgc | tgg | atc | 3885 | |
| Asn | Glu | Ser | Gly | His | Gly | Ala | Asn | His | Asp | Ala | Leu | Tyr | Arg | Trp | Ile | | |
| | | | 485 | | | | | 490 | | | | | 495 | | | | |
| aaa | tct | gtc | gat | cct | tcc | cgc | ccg | gtg | cag | tat | gaa | ggc | ggc | gga | gcc | 3933 | |
| Lys | Ser | Val | Asp | Pro | Ser | Arg | Pro | Val | Gln | Tyr | Glu | Gly | Gly | Gly | Ala | | |
| | | 500 | | | | | 505 | | | | | 510 | | | | | |
| gac | acc | acg | gcc | acc | gat | att | att | tgc | ccg | atg | tac | gcg | cgc | gtg | gat | 3981 | |
| Asp | Thr | Thr | Ala | Thr | Asp | Ile | Ile | Cys | Pro | Met | Tyr | Ala | Arg | Val | Asp | | |
| | 515 | | | | | 520 | | | | | 525 | | | | | | |
| gaa | gac | cag | ccc | ttc | ccg | gct | gtg | ccg | aaa | tgg | tcc | atc | aaa | aaa | tgg | 4029 | |
| Glu | Asp | Gln | Pro | Phe | Pro | Ala | Val | Pro | Lys | Trp | Ser | Ile | Lys | Lys | Trp | | |
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| ctt | tcg | cta | cct | gga | gag | acg | cgc | ccg | ctg | atc | ctt | tgc | gaa | tac | gcc | 4077 | |
| Leu | Ser | Leu | Pro | Gly | Glu | Thr | Arg | Pro | Leu | Ile | Leu | Cys | Glu | Tyr | Ala | | |
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| cac | gcg | atg | ggc | aac | agt | ctt | ggc | ggc | ttc | gct | aaa | tac | tgg | cag | gcg | 4125 | |
| His | Ala | Met | Gly | Asn | Ser | Leu | Gly | Gly | Phe | Ala | Lys | Tyr | Trp | Gln | Ala | | |
| | | | 565 | | | | | 570 | | | | | 575 | | | | |
| ttt | cgt | cag | tat | ccc | cgt | tta | cag | ggc | ggc | ttc | gtc | tgg | gac | tgg | gtg | 4173 | |
| Phe | Arg | Gln | Tyr | Pro | Arg | Leu | Gln | Gly | Gly | Phe | Val | Trp | Asp | Trp | Val | | |

| 580 | 585 | 590 | |
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| gat cag tcg ctg att aaa tat gat gaa aac ggc aac ccg tgg tcg gct Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala 595 600 605 | | | 4221 |
| tac ggc ggt gat ttt ggc gat acg ccg aac gat cgc cag ttc tgt atg Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met 610 615 620 625 | | | 4269 |
| aac ggt ctg gtc ttt gcc gac cgc acg ccg cat cca gcg ctg acg gaa Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu 630 635 640 | | | 4317 |
| gca aaa cac cag cag cag ttt ttc cag ttc cgt tta tcc ggg caa acc Ala Lys His Gln Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr 645 650 655 | | | 4365 |
| atc gaa gtg acc agc gaa tac ctg ttc cgt cat agc gat aac gag ctc Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu 660 665 670 | | | 4413 |
| ctg cac tgg atg gtg gcg ctg gat ggt aag ccg ctg gca agc ggt gaa Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu 675 680 685 | | | 4461 |
| gtg cct ctg gat gtc gct cca caa ggt aaa cag ttg att gaa ctg cct Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro 690 695 700 705 | | | 4509 |
| gaa cta ccg cag ccg gag agc gcc ggg caa ctc tgg ctc aca gta cgc Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg 710 715 720 | | | 4557 |
| gta gtg caa ccg aac gcg acc gca tgg tca gaa gcc ggg cac atc agc Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser 725 730 735 | | | 4605 |
| gcc tgg cag cag tgg cgt ctg gcg gaa aac ctc agt gtg acg ctc ccc Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro 740 745 750 | | | 4653 |
| gcc gcg tcc cac gcc atc ccg cat ctg acc acc agc gaa atg gat ttt Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe 755 760 765 | | | 4701 |
| tgc atc gag ctg ggt aat aag cgt tgg caa ttt aac cgc cag tca ggc Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly 770 775 780 785 | | | 4749 |
| ttt ctt tca cag atg tgg att ggc gat aaa aaa caa ctg ctg acg ccg Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro 790 795 800 | | | 4797 |
| ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc gta Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val 805 810 815 | | | 4845 |
| agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg aag Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys 820 825 830 | | | 4893 |

| | |
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| gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg gca Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala 835 840 845 | 4941 |
| gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg cag Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln 850 855 860 865 | 4989 |
| cat cag ggg aaa acc tta ttt atc agc cgg aaa acc tac cgg att gat His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp 870 875 880 | 5037 |
| ggg agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc gat Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp 885 890 895 | 5085 |
| aca ccg cat ccg gcg cgg att ggc ctg aac tgc cag ctg gcg cag gta Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val 900 905 910 | 5133 |
| gca gag cgg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat ccc Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro 915 920 925 | 5181 |
| gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg tca Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser 930 935 940 945 | 5229 |
| gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc tgc Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys 950 955 960 | 5277 |
| ggg acg cgc gaa ttg aat tat ggc cca cac cag tgg cgc ggc gac ttc Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe 965 970 975 | 5325 |
| cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc agc Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser 980 985 990 | 5373 |
| cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc gac His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp 995 1000 1005 | 5421 |
| ggg ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser 1010 1015 1020 | 5466 |
| gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln 1025 1030 1035 | 5511 |
| ttg gtc tgg tgt caa aaa taa tgactgcagg tcgaccatag tgactggata Leu Val Trp Cys Gln Lys 1040 1045 | 5562 |
| tggtgtgttt tacagtatta tgtagtctgt tttttatgca aaatctaatt taatatattg | 5622 |
| atatttatat cattttacgt ttctcgttca gctttcttgt acaaagtggg gagaatgaat | 5682 |

gaagatctg ggg aag cct atc cct aac cct ctc ctc ggt ctc gat tct 5730
 Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
 1050 1055

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 Thr Arg Thr Gly His His His His His His
 1060 1065

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 <211> 21
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mel/V5-His DEST cassette

<400> 95

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Ser Tyr Ile Tyr Ala
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<210> 96
 <211> 1024
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mel/V5-His DEST cassette

<400> 96

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Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro
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Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
 35 40 45

Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Arg Phe Ala Trp Phe
 50 55 60

Pro Ala Pro Glu Ala Val Pro Glu Ser Trp Leu Glu Cys Asp Leu Pro
 65 70 75 80

Glu Ala Asp Thr Val Val Val Pro Ser Asn Trp Gln Met His Gly Tyr
 85 90 95

Asp Ala Pro Ile Tyr Thr Asn Val Thr Tyr Pro Ile Thr Val Asn Pro
100 105 110

Pro Phe Val Pro Thr Glu Asn Pro Thr Gly Cys Tyr Ser Leu Thr Phe
115 120 125

Asn Val Asp Glu Ser Trp Leu Gln Glu Gly Gln Thr Arg Ile Ile Phe
130 135 140

Asp Gly Val Asn Ser Ala Phe His Leu Trp Cys Asn Gly Arg Trp Val
145 150 155 160

Gly Tyr Gly Gln Asp Ser Arg Leu Pro Ser Glu Phe Asp Leu Ser Ala
165 170 175

Phe Leu Arg Ala Gly Glu Asn Arg Leu Ala Val Met Val Leu Arg Trp
180 185 190

Ser Asp Gly Ser Tyr Leu Glu Asp Gln Asp Met Trp Arg Met Ser Gly
195 200 205

Ile Phe Arg Asp Val Ser Leu Leu His Lys Pro Thr Thr Gln Ile Ser
210 215 220

Asp Phe His Val Ala Thr Arg Phe Asn Asp Asp Phe Ser Arg Ala Val
225 230 235 240

Leu Glu Ala Glu Val Gln Met Cys Gly Glu Leu Arg Asp Tyr Leu Arg
245 250 255

Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln Val Ala Ser Gly Thr
260 265 270

Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg Gly Gly Tyr Ala Asp
275 280 285

Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro Lys Leu Trp Ser Ala
290 295 300

Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu Leu His Thr Ala Asp
305 310 315 320

Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val Gly Phe Arg Glu Val
325 330 335

Arg Ile Glu Asn Gly Leu Leu Leu Leu Asn Gly Lys Pro Leu Leu Ile

| 340 | 345 | 350 |
|--|-----|---------|
| Arg Gly Val Asn Arg His Glu His His Pro Leu His Gly Gln Val Met 355 | 360 | 365 |
| Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu Met Lys Gln Asn Asn 370 | 375 | 380 |
| Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn His Pro Leu Trp Tyr 385 | 390 | 395 400 |
| Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val Asp Glu Ala Asn Ile 405 | 410 | 415 |
| Glu Thr His Gly Met Val Pro Met Asn Arg Leu Thr Asp Asp Pro Arg 420 | 425 | 430 |
| Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg Met Val Gln Arg Asp 435 | 440 | 445 |
| Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu Gly Asn Glu Ser Gly 450 | 455 | 460 |
| His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp Ile Lys Ser Val Asp 465 | 470 | 475 480 |
| Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly Gly Ala Asp Thr Thr Ala 485 | 490 | 495 |
| Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val Asp Glu Asp Gln Pro 500 | 505 | 510 |
| Phe Pro Ala Val Pro Lys Trp Ser Ile Lys Lys Trp Leu Ser Leu Pro 515 | 520 | 525 |
| Gly Glu Thr Arg Pro Leu Ile Leu Cys Glu Tyr Ala His Ala Met Gly 530 | 535 | 540 |
| Asn Ser Leu Gly Gly Phe Ala Lys Tyr Trp Gln Ala Phe Arg Gln Tyr 545 | 550 | 555 560 |
| Pro Arg Leu Gln Gly Gly Phe Val Trp Asp Trp Val Asp Gln Ser Leu 565 | 570 | 575 |
| Ile Lys Tyr Asp Glu Asn Gly Asn Pro Trp Ser Ala Tyr Gly Gly Asp 580 | 585 | 590 |

Phe Gly Asp Thr Pro Asn Asp Arg Gln Phe Cys Met Asn Gly Leu Val
595 600 605

Phe Ala Asp Arg Thr Pro His Pro Ala Leu Thr Glu Ala Lys His Gln
610 615 620

Gln Gln Phe Phe Gln Phe Arg Leu Ser Gly Gln Thr Ile Glu Val Thr
625 630 635 640

Ser Glu Tyr Leu Phe Arg His Ser Asp Asn Glu Leu Leu His Trp Met
645 650 655

Val Ala Leu Asp Gly Lys Pro Leu Ala Ser Gly Glu Val Pro Leu Asp
660 665 670

Val Ala Pro Gln Gly Lys Gln Leu Ile Glu Leu Pro Glu Leu Pro Gln
675 680 685

Pro Glu Ser Ala Gly Gln Leu Trp Leu Thr Val Arg Val Val Gln Pro
690 695 700

Asn Ala Thr Ala Trp Ser Glu Ala Gly His Ile Ser Ala Trp Gln Gln
705 710 715 720

Trp Arg Leu Ala Glu Asn Leu Ser Val Thr Leu Pro Ala Ala Ser His
725 730 735

Ala Ile Pro His Leu Thr Thr Ser Glu Met Asp Phe Cys Ile Glu Leu
740 745 750

Gly Asn Lys Arg Trp Gln Phe Asn Arg Gln Ser Gly Phe Leu Ser Gln
755 760 765

Met Trp Ile Gly Asp Lys Lys Gln Leu Leu Thr Pro Leu Arg Asp Gln
770 775 780

Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly Val Ser Glu Ala Thr
785 790 795 800

Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp Lys Ala Ala Gly His
805 810 815

Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr Ala Asp Thr Leu Ala
820 825 830

Asp Ala Val Leu Ile Thr Thr Ala His Ala Trp Gln His Gln Gly Lys
835 840 845

Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile Asp Gly Ser Gly Gln
850 855 860

Met Ala Ile Thr Val Asp Val Glu Val Ala Ser Asp Thr Pro His Pro
865 870 875 880

Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln Val Ala Glu Arg Val
885 890 895

Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr Pro Asp Arg Leu Thr
900 905 910

Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu Ser Asp Met Tyr Thr
915 920 925

Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg Cys Gly Thr Arg Glu
930 935 940

Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp Phe Gln Phe Asn Ile
945 950 955 960

Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr Ser His Arg His Leu
965 970 975

Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile Asp Gly Phe His Met
980 985 990

Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser Val Ser Ala Glu Phe
995 1000 1005

Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu Val Trp Cys Gln
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Lys

<210> 97

<211> 23

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<223> Mel/V5-His DEST cassette

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1 5 10 15

Gly His His His His His His
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<210> 98

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<213> Unknown

<220>

<223> AcMNPV ORF 25 promoter sequence

<400> 98

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<210> 99

<211> 1033

<212> DNA

<213> Unknown

<220>

<223> AcMNPV lef 3 promoter

<400> 99

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| catttggatc gtttcgtgtt caaacgcgtc gaaaactttt aaaacgcaat tgccgccggg | 120 |
| acgcaggcaa attaaaatta gctgcgtctc gcacatgatc aaatcaaagt tgagacgttc | 180 |
| ttgttcgttt tcgcgtccat taacgtcaac cgagccatct gccaacacca gatcgcacgc | 240 |
| gttgccacac ttgatgctaa tctcaaatac aacattttta tcaaacacgt cgcctgactt | 300 |
| gtcggggcccc gtaatggttg tgaaattttt gcgtttgccg actgtcgggt tgtacacgca | 360 |
| caccgagttg tttgtcaacg tgacgccata cgctttgcaa agcgggttca acgacatggt | 420 |
| atagttggca aactcgcccg gtccgccgca caaatccaaa aacgtgtcaa cgtgtcggca | 480 |
| aacgtgaaac tttttgtcga tctctgatag ttttcgcca catctaggtc tgcgcgttgg | 540 |
| gcgtttgtca aataattttg agcgagcgca aaccaccgac ttgctgctga acgtgttcaa | 600 |
| accatctttg agtttattta atttttgctg caacattttt actcttcgtg tcggtcgcaa | 660 |
| tgtttgtgtc gaaaaagacg gccaacacgc tcagcaaaac tatacaaata aagaacaaaa | 720 |
| atacgtacgc aatattaaca ttgaccgttt gatcgttaaa tcggacgggt ctgttcagag | 780 |
| ccgctcttat tctctcgttg tacattgtta aagtttttgt ttttaaattg tacacaatcg | 840 |
| gcgtgttgta gtcgaaattt tcaaaatcgg ctttttgaaa cattgttctg aacgtgttgt | 900 |
| cgagcggcgt gttgctggcc acgtttataa tcaactccct ccacgctaac gaacgggtgt | 960 |
| ctggcgacac ttcgatttcg tcgccattca gtatttgcca tcggatagat tcccacatat | 1020 |
| cgacaacagc aat | 1033 |

<210> 100

<211> 1053

<212> DNA

<213> Unknown

<220>

<223> AcMNPV TLP promoter

<400> 100

| | |
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| tgctagccca attggccact gttgtacgaa atatcgtcgt caacgtgttt gaatacatgt | 60 |
| tggcccgtag cgttgggtaa atctatgcat ctggagtcgc cggaacactc gtactggttg | 120 |
| tcagagtttc tgatccgggt gatgcacggt atcagttgtg actcgttatt attcaaakat | 180 |
| ttgaaatatt gcgtgtcgcc gatatcggcc gttatgtacg tgtgtccggc gccgttaaac | 240 |
| gcgcacggat gcgcttcac gcacgacatt aagttgcgat caaatatttt attcgcgggg | 300 |
| cattcgccca ccacgtggcg ccattttacg cactgcataa actggttgac gagcaaattg | 360 |

gagggaaagt atgatagtat atagccgtct ggcoctgtttt cacacaattc gttaacttta 420
cactggccgg tttccgcgtc aaacgtgtaa ttatctggac attcttcgac tgcgtgcgct 480
ccgtttgcaa aacacctaag atagaacgtg ggatgatata agtgcgcggtt ggtagaataa 540
tctttgtcca agtggttggt caacaccaac gtgtccagca aacgctcgtc catgggataa 600
agaccggcag acttggtgtc gcacggcggc acgggaacac attttagttg tgcgtaatca 660
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aatttttgat ttaagaaatc aaaaatttca atccggtcat catgcacgct ttcgtgatag 840
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acgtagccta ttacgtcggg tgtgggttcg tctgcgttgg tgcgcttcac atattcagtc 960
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attaaagtaa acgctattat aagaaaaaag ctt 1053

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<211> 507
<212> DNA
<213> Unknown

<220>
<223> AcMNPV hr5 sequence

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gacatcagct tttattttta taacaaatga catcatttct tgattgtgtt ttacacgtag 120
aattctactc gtaaagcgag ttcagttttg aaaaacaaat gacatcatct ttttgattgt 180
gctttacaag tagaattcta cccgtaaata aagttcgggt ttgaaaaaca aatgagtcac 240
attgtatgat atcatattgc aaacaaatga ctcatcaatc gatcgtgcgt acacgtagaa 300
ttctactcgt aaagcgagtt tatgagccgt gtgcaaaaca tgacatcatc tcgatttgaa 360
aaacaaatga catcatccac tgatcgtgcg ttacaagtag aattctactc gtaaagccag 420
ttcggttatg agccgtgtgc aaaacatgac atcagcttat gactcgtact tgattgtgtt 480
ttacgcgtag aattctactc gtaaagc 507

<210> 102
<211> 507
<212> DNA
<213> Unknown

<220>
<223> AcMNPV IE-1 promoter

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gacatcagct tttattttta taacaaatga catcatttct tgattgtggt ttacacgtag 120
aattctactc gtaaagcgag ttcagttttg aaaaacaaat gacatcatct ttttgattgt 180
gctttacaag tagaattcta cccgtaaate aagttcgggt ttgaaaaaca aatgagtcac 240
attgtatgat atcatattgc aaacaaatga ctcatcaatc gatcgtgcgt acacgtagaa 300
ttctactcgt aaagcgagtt tatgagccgt gtgcaaaaca tgacatcatc tcgatttgaa 360
aaacaaatga catcatccac tgatcgtgcg ttacaagtag aattctactc gtaaagccag 420
ttcgggttatg agccgtgtgc aaaacatgac atcagcttat gactcgtact tgattgtggt 480
ttacgcgtag aattctactc gtaaagc 507

<210> 103
<211> 1746
<212> DNA
<213> Unknown

<220>
<223> AcMPNV IE-1 coding sequence

<400> 103
atgacgcaaa ttaattttta cgcgtcgtac accagcgctt cgacgccgtc ccgagcgctc 60
ttcgacaaca gctattcaga gttttgtgat aaacaacca acgactatct aagttattat 120
aaccatccca ccccgatg agccgacacg gtgatattct acagcgagac tgcggcagct 180
tcaaactttt tggcaagcgt caactcgtta actgataatg atttagtgga atgtttgctc 240
aagaccactg ataattctga agaagcagtt agttctgctt attattcgga atcccttgag 300
cagcctgttg tggagcaacc atcgcccagt tctgcttatc atgcggaatc ttttgagcat 360
tctgctggtg tgaaccaacc atcggcaact ggaactaaac ggaagctgga cgaataactg 420
gacaattcac aaggtgtggt gggccagttt aacaaaatta aattgaggcc taaatacaag 480
aaaagcacia ttcaaagctg tgcaaccctt gaacagacaa ttaatcacia cacgaacatt 540
tgcacggtcg cttcaactca agaaattacg cattatttta ctaatgattt tgcgccgtat 600
ttaatgcgtt tcgacgacaa cgactacaat tccaacaggt tctccgacca tatgtccgaa 660
actggttatt acatgtttgt ggttaaaaaa agtgaagtga agccgtttga aattatatct 720
gccaaagtac tgagcaatgt ggtttacgaa tatacaaaac attattacat ggtagataat 780
cgcgtgtttg tggttaacttt tgataaaatt aggtttatga tttcgtacaa tttggttaaa 840
gaaaccggca tagaaattcc tcattctcaa gatgtgtgca acgacgagac ggctgcacaa 900
aattgtaaaa aatgccattt cgtcgatgtg caccacacgt ttaaagctgc tctgacttca 960

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tattttaatt tagatatgta ttacgcgcaa accacatttg tgactttgtt acaatcgttg 1020
ggcgaaagaa aatgtggggt tcttttgagc aagttgtacg aaatgtatca agataaaaat 1080
ttattttactt tgcctattat gcttagtcgt aaagagagta atgaaattga gactgcatct 1140
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ttgtccgacg ctataacggt tgcggaacaa aaactaaatt gtaaataataa aaaattcgaa 1740
tttaat 1746

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<210> 104
<211> 582
<212> PRT
<213> Unknown

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<220>
<223> AcMNPV IE-1 protein sequence

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<400> 104

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Met Thr Gln Ile Asn Phe Asn Ala Ser Tyr Thr Ser Ala Ser Thr Pro
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```

Ser Arg Ala Ser Phe Asp Asn Ser Tyr Ser Glu Phe Cys Asp Lys Gln
          20           25           30

```

```

Pro Asn Asp Tyr Leu Ser Tyr Tyr Asn His Pro Thr Pro Asp Gly Ala
          35           40           45

```

```

Asp Thr Val Ile Ser Asp Ser Glu Thr Ala Ala Ala Ser Asn Phe Leu
          50           55           60

```

```

Ala Ser Val Asn Ser Leu Thr Asp Asn Asp Leu Val Glu Cys Leu Leu
          65           70           75           80

```

```

Lys Thr Thr Asp Asn Leu Glu Glu Ala Val Ser Ser Ala Tyr Tyr Ser

```


| 85 | | | | | | | 90 | | | | | | | 95 | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| Glu | Ser | Leu | Glu | Gln | Pro | Val | Val | Glu | Gln | Pro | Ser | Pro | Ser | Ser | Ala | | | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | | | |
| Tyr | His | Ala | Glu | Ser | Phe | Glu | His | Ser | Ala | Gly | Val | Asn | Gln | Pro | Ser | | | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | | | |
| Ala | Thr | Gly | Thr | Lys | Arg | Lys | Leu | Asp | Glu | Tyr | Leu | Asp | Asn | Ser | Gln | | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | | | |
| Gly | Val | Val | Gly | Gln | Phe | Asn | Lys | Ile | Lys | Leu | Arg | Pro | Lys | Tyr | Lys | | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | | |
| Lys | Ser | Thr | Ile | Gln | Ser | Cys | Ala | Thr | Leu | Glu | Gln | Thr | Ile | Asn | His | | | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | | | |
| Asn | Thr | Asn | Ile | Cys | Thr | Val | Ala | Ser | Thr | Gln | Glu | Ile | Thr | His | Tyr | | | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | | | |
| Phe | Thr | Asn | Asp | Phe | Ala | Pro | Tyr | Leu | Met | Arg | Phe | Asp | Asp | Asn | Asp | | | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | | | |
| Tyr | Asn | Ser | Asn | Arg | Phe | Ser | Asp | His | Met | Ser | Glu | Thr | Gly | Tyr | Tyr | | | | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | | | | |
| Met | Phe | Val | Val | Lys | Lys | Ser | Glu | Val | Lys | Pro | Phe | Glu | Ile | Ile | Phe | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | | |
| Ala | Lys | Tyr | Val | Ser | Asn | Val | Val | Tyr | Glu | Tyr | Thr | Asn | Asn | Tyr | Tyr | | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | | |
| Met | Val | Asp | Asn | Arg | Val | Phe | Val | Val | Thr | Phe | Asp | Lys | Ile | Arg | Phe | | | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | | | |
| Met | Ile | Ser | Tyr | Asn | Leu | Val | Lys | Glu | Thr | Gly | Ile | Glu | Ile | Pro | His | | | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | | | |
| Ser | Gln | Asp | Val | Cys | Asn | Asp | Glu | Thr | Ala | Ala | Gln | Asn | Cys | Lys | Lys | | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | | |
| Cys | His | Phe | Val | Asp | Val | His | His | Thr | Phe | Lys | Ala | Ala | Leu | Thr | Ser | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | | |
| Tyr | Phe | Asn | Leu | Asp | Met | Tyr | Tyr | Ala | Gln | Thr | Thr | Phe | Val | Thr | Leu | | | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | | | |

Leu Gln Ser Leu Gly Glu Arg Lys Cys Gly Phe Leu Leu Ser Lys Leu
340 345 350

Tyr Glu Met Tyr Gln Asp Lys Asn Leu Phe Thr Leu Pro Ile Met Leu
355 360 365

Ser Arg Lys Glu Ser Asn Glu Ile Glu Thr Ala Ser Asn Asn Phe Phe
370 375 380

Val Ser Pro Tyr Val Ser Gln Ile Leu Lys Tyr Ser Glu Ser Val Gln
385 390 395 400

Phe Pro Asp Asn Pro Pro Asn Lys Tyr Val Val Asp Asn Leu Asn Leu
405 410 415

Ile Val Asn Lys Lys Ser Thr Leu Thr Tyr Lys Tyr Ser Ser Val Ala
420 425 430

Asn Leu Leu Phe Asn Asn Tyr Lys Tyr His Asp Asn Ile Ala Ser Asn
435 440 445

Asn Asn Ala Glu Asn Leu Lys Lys Val Lys Lys Glu Asp Gly Ser Met
450 455 460

His Ile Val Glu Gln Tyr Leu Thr Gln Asn Val Asp Asn Val Lys Gly
465 470 475 480

His Asn Phe Ile Val Leu Ser Phe Lys Asn Glu Glu Arg Leu Thr Ile
485 490 495

Ala Lys Lys Asn Lys Glu Phe Tyr Trp Ile Ser Gly Glu Ile Lys Asp
500 505 510

Val Asp Val Ser Gln Val Ile Gln Lys Tyr Asn Arg Phe Lys His His
515 520 525

Met Phe Val Ile Gly Lys Val Asn Arg Arg Glu Ser Thr Thr Leu His
530 535 540

Asn Asn Leu Leu Lys Leu Leu Ala Leu Ile Leu Gln Gly Leu Val Pro
545 550 555 560

Leu Ser Asp Ala Ile Thr Phe Ala Glu Gln Lys Leu Asn Cys Lys Tyr
565 570 575

Lys Lys Phe Glu Phe Asn
580

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<212> DNA
<213> Artificial Sequence

<220>
<223> pLenti6/V5-DEST

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aacagggact tgaaagcgaa agggaaacca gaggagctct ctcgacgcag gactcggctt 480
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aaacatatag tatgggcaag caggagctga gaacgattcg cagttaatcc tggcctgtta 720
gaaacatcag aaggctgtag acaaatactg ggacagctac aaccatccct tcagacagga 780
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| | |
|---|------|
| ttacacaagc ttaatacact ccttaattga agaatcgcaa aaccagcaag aaaagaatga | 1500 |
| acaagaatta ttggaattag ataaatgggc aagtttgtgg aattggttta acataacaaa | 1560 |
| ttggctgtgg tatataaaat tattcataat gatagtagga ggcttggtag gtttaagaat | 1620 |
| agtttttgcgt gtactttcta tagtgaatag agttaggcag ggatattcac cattatcggt | 1680 |
| tcagacccac ctccaaccc cgaggggacc cgacaggccc gaaggaatag aagaagaagg | 1740 |
| tggagagaga gacagagaca gatccattcg attagtgaac ggatctcgac ggtatcgata | 1800 |
| agcttgggag ttccgcgtta cataacttac ggtaaattggc ccgcctggct gaccgccccaa | 1860 |
| cgacccccgc ccattgacgt caataatgac gtatgttccc atagtaacgc caatagggac | 1920 |
| tttccattga cgtcaatggg tggagtattt acggtaaact gccacttgg cagtacatca | 1980 |
| agtgtatcat atgccaagta cgcacctat tgacgtcaat gacggtaaatt ggcccgctg | 2040 |
| gcattatgcc cagtacatga ccttatggga ctttctact tggcagtaca tctacgtatt | 2100 |
| agtcacgct attaccatgg tgatgcggtt ttggcagtac atcaatgggc gtggatagcg | 2160 |
| gtttgactca cggggatttc caagtctcca cccattgac gtcaatggga gtttgttttg | 2220 |
| gcacaaaaat caacgggact ttcaaaaatg tcgtaacaac tccgccccat tgacgcaa | 2280 |
| ggcggtagg cgtgtacggt gggaggctta tataagcaga gctcgtttag tgaaccgtca | 2340 |
| gatcgctgg agacgccatc cacgctgttt tgacctccat agaagacacc gactctagag | 2400 |
| gatccactag tccagtgtgg tggaaattctg cagatatcaa caagtttgta caaaaaagct | 2460 |
| gaacgagaaa cgtaaaatga tataaatatc aatatattaa attagatttt gcataaaaaa | 2520 |
| cagactacat aatactgtaa aacacaacat atccagtcac tatggcgggc gcattaggca | 2580 |
| ccccaggctt tacactttat gcttccggct cgtataatgt gtggattttg agttaggatc | 2640 |
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| aaaataagca caagttttat ccggccttta ttcacattct tgcgcgctg atgaatgctc | 2880 |
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| acgacgattt ccggcagttt ctacacatat attcgcaaga tgtggcgtgt tacggtgaaa | 3060 |
| acctggccta tttccctaaa gggtttattg agaatatgtt tttcgtctca gccaatccct | 3120 |
| gggtgagttt caccagtttt gatttaaacg tggccaatat ggacaacttc ttcgccccg | 3180 |
| ttttcaccat gggcaaatat tatacgcaag gcgacaaggt gctgatgccg ctggcgattc | 3240 |

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|------|
| aggttcatca | tgccgtctgt | gatggcttcc | atgtcggcag | aatgcttaat | gaattacaac | 3300 |
| agtactgcga | tgagtggcag | ggcggggcgt | aaagatctgg | atccggctta | ctaaaagcca | 3360 |
| gataacagta | tgcgatattg | cgcgctgatt | tttgcggtat | aagaatatat | actgatatgt | 3420 |
| atacccgaag | tatgtcaaaa | agaggtgtgc | tatgaagcag | cgtattacag | tgacagttga | 3480 |
| cagcgacagc | tatcagttgc | tcaaggcata | tatgatgtca | atatctccgg | tctggtaagc | 3540 |
| acaaccatgc | agaatgaagc | ccgtcgtctg | cgtgccgaac | gctggaaagc | ggaaaatcag | 3600 |
| gaagggatgg | ctgaggtcgc | ccggtttatt | gaaatgaacg | gctcttttgc | tgacgagaac | 3660 |
| agggactggg | gaaatgcagt | ttaaggttta | cacctataaa | agagagagcc | gttatcgtct | 3720 |
| gtttgtggat | gtacagagtg | atattattga | cacgcccggg | cgacggatgg | tgatccccct | 3780 |
| ggccagtgca | cgtctgctgt | cagataaagt | ctcccgtgaa | ctttaccggg | tggtgcatat | 3840 |
| cggggatgaa | agctggcgca | tgatgaccac | cgatatggcc | agtgtgccgg | tctccgttat | 3900 |
| cggggaagaa | gtggctgata | tcagccaccg | cgaaaatgac | atcaaaaacg | ccattaacct | 3960 |
| gatgttctgg | ggaatataaa | tgtcaggctc | cgttatacac | agccagtctg | caggtcgacc | 4020 |
| atagtgactg | gatatgttgt | gttttacagt | attatgtagt | ctgtttttta | tgcaaaatct | 4080 |
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| caggcagaag | tatgcaaagc | atgcatctca | attagtcagc | aaccagggtg | ggaaagtccc | 4380 |
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| Ile | Leu | Glu | Ser | Phe | Arg | Pro | Glu | Glu | Arg | Phe | Pro | Met | Met | Ser | Thr | 35 | 40 | 45 |
| Phe | Lys | Val | Leu | Leu | Cys | Gly | Ala | Val | Leu | Ser | Arg | Asp | Asp | Ala | Gly | 50 | 55 | 60 |
| Gln | Glu | Gln | Leu | Gly | Arg | Arg | Ile | His | Tyr | Ser | Gln | Asn | Asp | Leu | Val | 65 | 70 | 75 |
| Glu | Tyr | Ser | Pro | Val | Thr | Glu | Lys | His | Leu | Thr | Asp | Gly | Met | Thr | Val | 85 | 90 | 95 |
| Arg | Glu | Leu | Cys | Ser | Ala | Ala | Ile | Thr | Met | Ser | Asp | Asn | Thr | Ala | Ala | 100 | 105 | 110 |
| Asn | Leu | Leu | Leu | Thr | Thr | Ile | Gly | Gly | Pro | Lys | Glu | Leu | Thr | Ala | Phe | 115 | 120 | 125 |
| Leu | His | Asn | Met | Gly | Asp | His | Val | Thr | Arg | Leu | Asp | His | Trp | Glu | Pro | 130 | 135 | 140 |
| Glu | Leu | Asn | Glu | Ala | Ile | Pro | Asn | Asp | Glu | Arg | Asp | Thr | Thr | Met | Pro | 145 | 150 | 155 |
| Val | Ala | Met | Ala | Thr | Thr | Leu | Arg | Lys | Leu | Leu | Thr | Gly | Glu | Leu | Leu | 165 | 170 | 175 |
| Thr | Leu | Ala | Ser | Arg | Gln | Gln | Leu | Ile | Asp | Trp | Met | Glu | Ala | Asp | Lys | 180 | 185 | 190 |
| Val | Ala | Gly | Pro | Leu | Leu | Arg | Ser | Ala | Leu | Pro | Ala | Gly | Trp | Phe | Ile | 195 | 200 | 205 |
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| Ala | Leu | Gly | Pro | Asp | Gly | Lys | Pro | Ser | Arg | Ile | Val | Val | Ile | Tyr | Thr | 225 | 230 | 235 |
| Thr | Gly | Ser | Gln | Ala | Thr | Met | Asp | Glu | Arg | Asn | Arg | Gln | Ile | Ala | Glu | 245 | 250 | 255 |

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<220>

<223> Nucleic acid fragment containing the tetracycline repressor coding sequence

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| acgttcgccc | gctttccccg | tcaagctcta | aatcgggggc | tccctttagg | gttccgattt | 4560 |
| agtgccttac | ggcacctcga | ccccaaaaaa | cttgattagg | gtgatgggtc | acgtagtggg | 4620 |
| ccatcgccct | gatagacggg | ttttcgccct | ttgacgttgg | agtccacgtt | ctttaatagt | 4680 |
| ggactcttgt | tccaaactgg | aacaacactc | aaccctatct | cggtctattc | ttttgattta | 4740 |
| taagggaatt | tgccgatttc | ggcctatttg | ttaaaaaatg | agctgattta | acaaaaattt | 4800 |
| aacgcgaatt | ttaacaaaat | attaacgttt | acaatttccc | aggtggcact | tttcggggaa | 4860 |
| atgtgcgcgg | aacccttatt | tgttttattt | tctaaataca | ttcaaataatg | tatccgctca | 4920 |
| tgagacaata | accctgataa | atgcttcaat | aatattgaaa | aaggaagagt | atgagtattc | 4980 |
| aacatttccg | tgtcgccttc | attccctttt | ttgcggcatt | ttgccttcct | gtttttgctc | 5040 |
| accagaaac | gctgggtgaa | gtaaaagatg | ctgaagatca | gttgggtgca | cgagtgggtt | 5100 |
| acatcgaact | ggatctcaac | agcggtaaga | tccttgagag | ttttcgcccc | gaagaacgtt | 5160 |
| ttccaatgat | gagcactttt | aaagttctgc | tatgtggcgc | ggtattatcc | cgtattgacg | 5220 |
| ccgggcaaga | gcaactcggt | cgccgcatac | actattctca | gaatgacttg | gttgagtact | 5280 |
| caccagtcac | agaaaagcat | cttacggatg | gcatgacagt | aagagaatta | tgcagtgtgt | 5340 |

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|------|
| ccataacat | gagtataac | actgaggcca | acttacttct | gacaacgatc | ggaggaccga | 5400 |
| aggagctaac | cgcttttttg | cacaacatgg | gggatcatgt | aactcgcctt | gatcggtggg | 5460 |
| aaccggagct | gaatgaagcc | ataccaaacg | acgagcgtga | caccacgatg | cctgtagcaa | 5520 |
| tggcaacaac | gttgcgcaaa | ctattaactg | gcgaactact | tactctagct | tcccggcaac | 5580 |
| aattaataga | ctggatggag | gcggataaag | ttgcaggacc | acttctgcgc | tcggcccttc | 5640 |
| cggctggctg | gtttattgct | gataaatctg | gagccggtga | gcgtgggtct | cgcggtatca | 5700 |
| ttgcagcact | ggggccagat | ggtaagccct | cccgtatcgt | agttatctac | acgacgggga | 5760 |
| gtcaggcaac | tatggatgaa | cgaaatagac | agatcgctga | gatagggtgcc | tcaactgatta | 5820 |
| agcattggta | actgtcagac | caagtttact | catatatact | ttagattgat | ttaaaacttc | 5880 |
| atttttaatt | taaaaggatc | taggtgaaga | tcctttttga | taatctcatg | acccaaatcc | 5940 |
| cttaacgtga | gttttcgttc | cactgagcgt | cagaccccg | agaaaagatc | aaaggatcct | 6000 |
| cttgagatcc | tttttttctg | cgcgtaatat | gctgcttgca | aacaaaaaaaa | ccaccgctac | 6060 |
| cagcgggtgt | ttgtttgccc | gatcaagagc | taccaactct | ttttccgaag | gtaactggct | 6120 |
| tcagcagagc | gcagatacca | aatactgtcc | ttctagtgtg | gccgtagtta | ggccaccact | 6180 |
| tcaagaactc | tgtagcaccg | cctacatacc | tcgctctgct | aatcctgtta | ccagtggctg | 6240 |
| ctgccagtgg | cgataagtcg | tgtcttaccg | ggttggactc | aagacgatag | ttaccggata | 6300 |
| aggcgcagcg | gtcgggctga | acgggggggt | cgtgcacaca | gccagcttg | gagcgaacga | 6360 |
| cctacaccga | actgagatac | ctacagcgtg | agctatgaga | aagcgccacg | cttcccgaag | 6420 |
| ggagaaaggc | ggacaggtat | ccggtaagcg | gcagggtcgg | aacaggagag | cgcacgaggg | 6480 |
| agcttccagg | gggaaacgcc | tggtatcttt | atagtcctgt | cgggtttcgc | cacctctgac | 6540 |
| ttgagcgtcg | atttttgtga | tgctcgtcag | gggggcggag | cctatggaaa | aacgccagca | 6600 |
| acgcggcctt | tttacggttc | ctggcctttt | gctggccttt | tgctcacatg | ttctttcctg | 6660 |
| cgttatcccc | tgattctgtg | gataaccgta | ttaccgcctt | tgagttagct | gataaccgctc | 6720 |
| gccgcagccg | aacgaccgag | cgcagcgagt | cagttagcga | ggaagcggaa | gagcgcccaa | 6780 |
| tacgcaaacc | gcctctcccc | gcgcgttggc | cgattcatta | atgcagctgg | cacgacaggt | 6840 |
| ttcccactg | gaaagcgggc | agttagcgca | acgcaattaa | tgtgagttag | ctcaactcatt | 6900 |
| aggcacccca | ggctttacac | tttatgcttc | cggctcgtat | gttggtgga | attgtgagcg | 6960 |
| gataacaatt | tcacacagga | aacagctatg | accatgatta | cgccaagcgc | gcaattaacc | 7020 |
| ctcactaaag | ggaacaaaag | ctggagctgc | aagctt | | | 7056 |

<211> 172
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pAd/CMV/V5-DEST

<220>
<221> misc_feature
<222> (172)..(172)
<223> n may be any nucleotide

<400> 121
ttgacgcaaa tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctctctgg 60
ctaactagag aaccactgc ttactggctt atcgaaatta atacgactca ctataggag 120
accaagctg gctagttaag ctatcaacaa gttgtacaa aaaagcaggc tn 172

<210> 122
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pAd/CMV/V5-DEST

<220>
<221> misc_feature
<222> (1)..(1)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (4)..(105)

<400> 122
nac cca gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg ttc 48
Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe
1 5 10 15
gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt 96
Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
20 25 30
acc ggt tag taatgagttt aaacggggga ggctaactga 135
Thr Gly

<210> 123
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombination region of pAd/CMV/V5-DEST

<400> 123

Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu
1 5 10 15

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
20 25 30

Gly

<210> 124

<211> 197

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombination region of pAd/PL-DEST

<220>

<221> misc_feature

<222> (197)..(197)

<223> n may be any nucleotide

<400> 124

tatttgtcta gggccgcggg gactttgacc gtttacgtgg agactcgccc aggtgttttt 60

ctcaggtggt ttccgcgttc cgggtcaaag ttggcgtttt attattatag tcagtcgaag 120

cttggatccg gtacctctag aattctcgag cggccgctag cgacatcgat cacaagtttg 180

tacaaaaaag caggctn 197

<210> 125

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombination region of pAd/PL-DEST

<220>

<221> misc_feature

<222> (1)..(1)

<223> n may be any nucleotide

<400> 125

naccagctt tcttgtacaa agtggtgatc gattcgacag atcactgaaa tgtgtgggcg 60

tggcttaagg gtgggaaaga atatataagg 90

<210> 126

<211> 560

<212> DNA

<213> Unknown

<220>

<223> OpIE2 promoter sequence

<400> 126

```
ggatcatgat gataaacaat gtatggtgct aatgttgctt caacaacaat tctgttgaac      60
tgtgttttca tgtttgccaa caagcacctt tatactcggg ggccctccca ccaccaactt      120
ttttgcactg caaaaaaaca cgcttttgca cgcgggccca tacatagtac aaactctacg      180
tttcgtagac tattttacat aaatagtcta caccgttgta tacgctcaa atacactacc      240
acacattgaa cctttttgca gtgcaaaaaa gtacgtgtcg gcagtcacgt aggccggcct      300
tatcgggtcg cgtcctgtca cgtacgaatc acattatcgg accggacgag tgttgtctta      360
tcgtgacagg acgccagctt cctgtgttgc taaccgcagc cggacgcaac tccttatcgg      420
aacaggacgc gcctccatat cagccgcgcg ttatctcatg cgcgtgaccg gacacgaggg      480
gcccgccccg cttatcgcgc ctataaatac agcccgaac gatctggtaa acacagttga      540
acagcatctg ttcgaattta                                         560
```

<210> 127

<211> 147

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombination region of pIB/V5-His-DEST

<220>

<221> misc_feature

<222> (141)..(148)

<223> n may be any nucleotide

<400> 127

```
cttatcgcgc ctataaatac agcccgaac gatctggtaa acacagttga acagcatctg      60
ttcgaattta aagcttgata tcgaattcct gcagcccagc gctggatcct cgatcacaag      120
tttgtacaaa aaagcaggct nnnnnnnn                                         147
```

<210> 128

<211> 184

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombination region of pIB/V5-His-DEST

<220>

<221> misc_feature

<222> (1)..(1)

)

<223> n may be any nucleotide

<220>

<221> CDS

<222> (4)..(135)

<400> 128

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| nac | cca | cca | gct | ttc | ttg | tac | aaa | gtg | gtg | atc | gac | ccg | ggg | cta | gag | 48 |
| | Pro | Pro | Ala | Phe | Leu | Tyr | Lys | Val | Val | Ile | Asp | Pro | Gly | Leu | Glu | |
| | 1 | | | | 5 | | | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ggc | ccg | cgg | ttc | gaa | ggg | aag | cct | atc | cct | aac | cct | ctc | ctc | ggg | ctc | 96 |
| Gly | Pro | Arg | Phe | Glu | Gly | Lys | Pro | Ile | Pro | Asn | Pro | Leu | Leu | Gly | Leu | |
| | | | | 20 | | | | 25 | | | | | | 30 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|-----|--|--|
| gat | tct | acg | cgt | acc | ggg | cat | cat | cac | cat | cac | cat | tga | gtttatctga | 145 | | |
| Asp | Ser | Thr | Arg | Thr | Gly | His | His | His | His | His | His | | | | | |
| | | | | 35 | | | | 40 | | | | | | | | |

| | | | | |
|------------|------------|------------|-----------|-----|
| ctaaatctta | ggtgtattgt | catgttttaa | tacaatatg | 184 |
|------------|------------|------------|-----------|-----|

<210> 129

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombination region of pIB/V5-His-DEST

<400> 129

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Ala | Phe | Leu | Tyr | Lys | Val | Val | Ile | Asp | Pro | Gly | Leu | Glu | Gly |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Phe | Glu | Gly | Lys | Pro | Ile | Pro | Asn | Pro | Leu | Leu | Gly | Leu | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| Ser | Thr | Arg | Thr | Gly | His | His | His | His | His | His | | | | | |
| | | | | 35 | | | | 40 | | | | | | | |

<210> 130

<211> 215

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombination region of pLenti6/V5-DEST

<220>

<221> misc_feature

<222> (215)..(215)

<223> n may be any nucleotide

<400> 130

| | | | | | | | |
|------------|------------|----------|----|------------|------------|------------|----|
| tcgtaacaac | tccgccccat | tgacgcaa | at | gggcggtagg | cgtgtacggt | gggaggtcta | 60 |
|------------|------------|----------|----|------------|------------|------------|----|

tataagcaga gctcggttag tgaaccgtca gatcgctgg agacgccatc cacgctgttt 120
 tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattctg 180
 cagatatcaa caagtttgta caaaaaagca ggctn 215

<210> 131
 <211> 142
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombination region of pLenti6/V5-DEST

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> n may be any nucleotide

<220>
 <221> CDS
 <222> (4)..(132)

<400> 131
 nac cca gct ttc ttg tac aaa gtg gtt gat atc cag cac agt ggc ggc 48
 Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly
 1 5 10 15
 cgc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct aac 96
 Arg Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn
 20 25 30
 cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag taatgagttt 142
 Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
 35 40

<210> 132
 <211> 42
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombination region of pLenti6/V5-DEST

<400> 132

Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly Arg
 1 5 10 15
 Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro
 20 25 30
 Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
 35 40

<210> 133
<211> 217
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of the expression clone resulting from
pLenti6/UbC/V5-DEST x entry clone

<220>
<221> misc_feature
<222> (217)..(217)
<223> n may be any nucleotide

<400> 133
ttggcgagtg tgttttgtga agtttttttag gcaccttttg aaatgtaatc atttgggtca 60
atatgtaatt ttcagtgtta gactagtaaa ttgtccgcta aattctggcc gtttttggct 120
tttttgtagt acgaagcttg gtaccgagct cggatccact agtccagtgt ggtggaattc 180
tgcagatatc aacaagtttg tacaataaag caggctn 217

<210> 134
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of the expression clone resulting from
pLenti6/UbC/V5-DEST x entry clone

<220>
<221> misc_feature
<222> (1)..(1)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (4)..(132)

<400> 134
nac cca gct ttc ttg tac aaa gtg gtt gat atc cag cac agt ggc ggc 48
Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly
1 5 10 15
cgc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct aac 96
Arg Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn
20 25 30
cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag taatgagttt 142
Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
35 40

<210> 135
<211> 42
<212> PRT

<213> Artificial Sequence

<220>

<223> Recombination region of the expression clone resulting from pLenti6/UbC/V5-DEST x entry clone

<400> 135

Pro Ala Phe Leu Tyr Lys Val Val Asp Ile Gln His Ser Gly Gly Arg
1 5 10 15

Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro
20 25 30

Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
35 40

<210> 136

<211> 1226

<212> DNA

<213> Unknown

<220>

<223> Sequence of the UbC promoter

<400> 136

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|-----|
| cggatctggc | ctccgcgcgcg | ggttttggcg | cctcccgcgcg | gcgccccct | cctcacggcg | 60 |
| agcgctgcca | cgtcagacga | agggcgcagg | agcgtcctga | tccttcgcgc | cggacgctca | 120 |
| ggacagcggc | ccgctgctca | taagactcgg | ccttagaacc | ccagtatcag | cagaaggaca | 180 |
| ttttaggacg | ggacttggtg | gactctaggg | cactggtttt | ctttccagag | agcggaacag | 240 |
| gcgaggaaaa | gtagtccctt | ctcggcgatt | ctgcggaggg | atctccgtgg | ggcggtgaa | 300 |
| gccgatgatt | atataaggac | gcgccgggtg | tggcacagct | agttccgtcg | cagccgggat | 360 |
| ttgggtcgcg | gttcttggtt | gtggatcgct | gtgatcgta | cttggtgagt | agcgggctgc | 420 |
| tgggctggcc | ggggctttcg | tggccgcgcg | gccgctcggt | gggacggaag | cgtgtggaga | 480 |
| gaccgccaag | ggctgtagtc | tgggtccgcg | agcaagggtg | ccctgaactg | ggggttgggg | 540 |
| ggagcgcagc | aaaatggcgc | ctgttcccca | gtcttgaatg | gaagacgctt | gtgaggcggg | 600 |
| ctgtgaggtc | gttgaaacaa | gggtgggggg | atggtgggcg | gcaagaacct | aaggctctga | 660 |
| ggccttcgct | aatgcgggaa | agctcttatt | cgggtgagat | gggctggggc | accatctggg | 720 |
| gaccctgacg | tgaagtttgt | cactgactgg | agaactcggt | ttgtcgtctg | ttgcgggggc | 780 |
| ggcagttatg | cgggtgccgt | gggcagtgca | ccgtacctt | tgggagcgcg | cgcctcgtc | 840 |
| gtgtcgtgac | gtcaccgcgt | ctgttggtt | ataatgcagg | gtggggccac | ctgccggtag | 900 |
| gtgtgcggta | ggctttttct | cgctgcagga | cgcagggttc | gggcctaggg | taggctctcc | 960 |


```
tgaatcgaca ggcgccggac ctctggtgag gggagggata agtgaggcgt cagtttcttt 1020
ggtcggtttt atgtacctat cttcttaagt agctgaagct ccggttttga actatgcgct 1080
cgggggttggc gagtgtgttt tgtgaagttt tttaggcacc ttttgaaatg taatcatttg 1140
ggccaatatg taatttttcag tgtagacta gtaaattgtc cgctaaattc tggccgtttt 1200
tggcctttttt gtttagacgaa gcttgg 1226
```

<210> 137
<211> 32
<212> DNA
<213> Unknown

<220>
<223> Directional cloning product of Figure 47

<220>
<221> misc_feature
<222> (13)..(27)
<223> N may be any nucleotide

<400> 137
cccttcacca tgnnnnnnnn nnnnnnnaag gg 32

<210> 138
<211> 192
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloning region of pLenti6/V5-D-Topo

```
<400> 138
tcgtaacaac tccgccccat tgacgcaa at gggcggtagg cgtgtacggt gggaggtcta 60
tataagcaga gctcgtttag tgaaccgtca gatcgcttgg agacgccatc cacgctgttt 120
tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattgat 180
cccttcacca tg 192
```

<210> 139
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloning region of pLenti6/V5-D-Topo

<220>
<221> CDS
<222> (1)..(87)

<400> 139

aag ggc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct 48
Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro
1 5 10 15

aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag taatgagttt 97
Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
20 25

ggaa 101

<210> 140
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Cloning region of pLenti6/V5-D-Topo

<400> 140

Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro
1 5 10 15

Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
20 25

<210> 141
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/V5-DEST

<220>
<221> misc_feature
<222> (166)..(166)
<223> n may be any nucleotide

<400> 141
caaatgggcg gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact 60

agagaaccca ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa 120

gctggctagt taagctatca acaagtttgt acaaaaaagc aggctn 166

<210> 142
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/V5-DEST

<220>

<221> misc_feature
<222> (4)..(4)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (7)..(108)

<400> 142
tagnac cca gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg 48
Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg
1 5 10

ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg 96
Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
15 20 25 30

cgt acc ggt tag taatgagttt aaacggggga ggctaactga aacacg 144
Arg Thr Gly

<210> 143
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/V5-DEST

<400> 143
Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu
1 5 10 15

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
20 25 30

Gly

<210> 144
<211> 166
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/GFP-DEST

<220>
<221> misc_feature
<222> (166)..(166)
<223> n may be any nucleotide

<400> 144
caaatgggacg gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact 60

agagaaccca ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa 120
gctggctagt taagctatca acaagtttgt acaaaaaagc aggctn 166

<210> 145
<211> 213
<212> DNA
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/GFP-DEST

<220>
<221> misc_feature
<222> (4)..(4)
<223> n may be any nucleotide

<220>
<221> CDS
<222> (7)..(213)

<400> 145
tagnac cca gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccc gcg 48
Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Ala
1 5 10

gct agc aaa gga gaa gaa ctt ttc act gga ggt gtc cca att ctt gtt 96
Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Gly Val Pro Ile Leu Val
15 20 25 30

gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga gag 144
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
35 40 45

ggt gaa ggt gat gct aca tac gga aag ctt acc ctt aaa ttt att tgc 192
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
50 55 60

act act gga aaa cta cct gtt 213
Thr Thr Gly Lys Leu Pro Val
65

<210> 146
<211> 69
<212> PRT
<213> Artificial Sequence

<220>
<223> Recombination region of pcDNA6.2/GFP-DEST

<400> 146

Pro Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Ala Ala Ser
1 5 10 15

Lys Gly Glu Glu Leu Phe Thr Gly Gly Val Pro Ile Leu Val Glu Leu
20 25 30

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
35 40 45

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
50 55 60

Gly Lys Leu Pro Val
65

<210> 147
<211> 307
<212> DNA
<213> Artificial

<220>
<223> Recombination region of pAd/CMV/V5 DEST

<220>
<221> misc_feature
<222> (172)..(173)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (176)..(277)

<400> 147
ttgacgcaaa tgggcggttag gcgtgtacgg tgggaggtct atataagcag agctctctgg 60
ctaactagag aaccactgc ttactggctt atcgaaatta atacgactca ctataggag 120
acccaagctg gctagttaag ctatcaacaa gtttgtacaa aaaagcaggc tnnac cca 178
Pro
1
gct ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg ttc gaa ggt 226
Ala Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu Gly
5 10 15
aag cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt 274
Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
20 25 30
tag taatgagttt aaacggggga ggctaactga 307

<210> 148
<211> 287
<212> DNA
<213> Artificial

<220>
<223> Recombination region of pAd/PL DEST

```
<220>
<221> misc_feature
<222> (197)..(198)
<223> n is a, c, g, or t

<400> 148
tatttgtcta gggccgcggg gactttgacc gtttacgtgg agactcgccc aggtgttttt      60
ctcaggtggt ttccgcgttc cgggtcaaag ttggcgtttt attattatag tcagtcgaag      120
cttggatccg gtacctctag aattctcgag cggccgctag cgacatcgat cacaagtttg      180
tacaaaaaag caggctnnac ccagctttct tgtacaaagt ggtgatcgat tcgacagatc      240
actgaaatgt gtgggcgtgg cttaaggggtg ggaaagaata tataagg                      287

<210> 149
<211> 325
<212> DNA
<213> Artificial

<220>
<223> Recombination region of pIB/V5 His DEST

<220>
<221> misc_feature
<222> (141)..(142)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (145)..(276)

<400> 149
cttatcgcg cttataaatac agcccgcaac gatctggtaa acacagttga acagcatctg      60
ttcgaattta aagcttgata tcgaattcct gcagcccagc gctggatcct cgatcacaag      120
tttgtacaaa aaagcaggct nnac cca cca gct ttc ttg tac aaa gtg gtg          171
                        Pro Pro Ala Phe Leu Tyr Lys Val Val
                        1                      5

atc gac ccg ggt cta gag ggc ccg cgg ttc gaa ggt aag cct atc cct          219
Ile Asp Pro Gly Leu Glu Gly Pro Arg Phe Glu Gly Lys Pro Ile Pro
10                      15                      20                      25

aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt cat cat cac cat          267
Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His
30                      35                      40

cac cat tga gtttatctga ctaaattctta gttgtattgt catgttttaa tacaatatg      325
His His

<210> 150
<211> 357
<212> DNA
<213> Artificial
```

<220>
<223> Recombination region of pLenti6/V5 DEST

<220>
<221> misc_feature
<222> (215)..(216)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (219)..(347)

<400> 150
tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta 60
tataagcaga gctcgtttag tgaaccgtca gatcgcttgg agacgccatc cacgctgttt 120
tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattctg 180
cagatatcaa caagtttgta caaaaaagca ggctnnac cca gct ttc ttg tac aaa 236
Pro Ala Phe Leu Tyr Lys
1 5
gtg gtt gat atc cag cac agt ggc ggc cgc tcg agt cta gag ggc ccg 284
Val Val Asp Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu Gly Pro
10 15 20
cgg ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat tct 332
Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
25 30 35
acg cgt acc ggt tag taatgagttt 357
Thr Arg Thr Gly
40

<210> 151
<211> 359
<212> DNA
<213> Artificial

<220>
<223> Recombination region of the expression clone resulting from
pLenti6/Ubc/V5 DEST x entry clone

<220>
<221> misc_feature
<222> (217)..(218)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (221)..(349)

<400> 151
ttggcgagtg tgttttgtga agtttttttag gcaccttttg aaatgtaatc atttgggtca 60
atatgtaatt ttcagtgtta gactagtaaa ttgtccgcta aattctggcc gtttttggct 120

```

tttttgtttag acgaagcttg gtaccgagct cggatccact agtccagtgt ggtggaattc      180
tgcagatatc aacaagtttg tacaaaaaag caggctnnac cca gct ttc ttg tac      235
                                     Pro Ala Phe Leu Tyr
                                     1                               5

aaa gtg gtt gat atc cag cac agt ggc ggc cgc tcg agt cta gag ggc      283
Lys Val Val Asp Ile Gln His Ser Gly Gly Arg Ser Ser Leu Glu Gly
                               10                               15                               20

ccg cgg ttc gaa ggt aag cct atc cct aac cct ctc ctc ggt ctc gat      331
Pro Arg Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
                               25                               30                               35

tct acg cgt acc ggt tag taatgagttt      359
Ser Thr Arg Thr Gly
                               40

```

```

<210> 152
<211> 293
<212> DNA
<213> Artificial

```

```

<220>
<223> Cloning region of pLenti6/V5 D Topo

```

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<220>
<221> CDS
<222> (193)..(279)

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```

<400> 152
tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt gggaggtcta      60
tataagcaga gtcggttttag tgaaccgtca gatcgccctgg agacgccatc cacgctgttt      120
tgacctccat agaagacacc gactctagag gatccactag tccagtgtgg tggaattgat      180
cccttcacca tg aag ggc tcg agt cta gag ggc ccg cgg ttc gaa ggt aag      231
                Lys Gly Ser Ser Leu Glu Gly Pro Arg Phe Glu Gly Lys
                1                               5                               10

cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag      279
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
                15                               20                               25

taatgagttt ggaa      293

```

```

<210> 153
<211> 310
<212> DNA
<213> Artificial

```

```

<220>
<223> Recombination region of pcDNA6.2/V5 DEST

```

```

<220>

```


<221> misc_feature
<222> (166)..(166)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (170)..(170)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (173)..(274)

<400> 153
caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact 60
agagaaccca ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa 120
gctggctagt taagctatca acaagtttgt acaaaaaagc aggctntagn ac cca gct 178
Pro Ala
1
ttc ttg tac aaa gtg gtt gat cta gag ggc ccg cgg ttc gaa ggt aag 226
Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Arg Phe Glu Gly Lys
5 10 15
cct atc cct aac cct ctc ctc ggt ctc gat tct acg cgt acc ggt tag 274
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
20 25 30
taatgagttt aaacggggga ggctaactga aacacg 310

<210> 154
<211> 379
<212> DNA
<213> Artificial

<220>
<223> Recombination region of pcDNA6.2/GFP DEST

<220>
<221> misc_feature
<222> (166)..(166)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (170)..(170)
<223> n is a, c, g, or t

<220>
<221> CDS
<222> (173)..(379)

<400> 154
caaatgggcg gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact 60
agagaaccca ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa 120

gctggctagt taagctatca acaagtttgt acaaaaaaagc aggcntnagn ac cca gct 178
Pro Ala
1

ttc ttg tac aaa gtg gtt gat cta gag ggc ccc gcg gct agc aaa gga 226
Phe Leu Tyr Lys Val Val Asp Leu Glu Gly Pro Ala Ala Ser Lys Gly
5 10 15

gaa gaa ctt ttc act gga ggt gtc cca att ctt gtt gaa tta gat ggt 274
Glu Glu Leu Phe Thr Gly Gly Val Pro Ile Leu Val Glu Leu Asp Gly
20 25 30

gat gtt aat ggg cac aaa ttt tct gtc agt gga gag ggt gaa ggt gat 322
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
35 40 45 50

gct aca tac gga aag ctt acc ctt aaa ttt att tgc act act gga aaa 370
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
55 60 65

cta cct gtt 379
Leu Pro Val

<210> 155
<211> 5
<212> DNA
<213> Artificial

<220>
<223> Topoisomerase recognition site

<220>
<221> misc_feature
<222> (1)..(1)
<223> n i s c o r t

<400> 155
ncctt 5

<210> 156
<211> 7
<212> DNA
<213> Artificial

<220>
<223> Topoisomerase recognition site for type IA E. coli topoisomerase
III

<400> 156
gcaactt 7

<210> 157
<211> 7
<212> DNA
<213> Artificial

<220>

<223> Overlap region; bases 6-12 in the core region

<400> 157

tttatac

7

<210> 158

<211> 7

<212> DNA

<213> Artificial

<220>

<223> Consensus sequence

<220>

<221> misc_feature

<222> (1)..(3)

<223> n is a, c, g, or t

<400> 158

nnnatac

7

<210> 159

<211> 7

<212> DNA

<213> Artificial

<220>

<223> Kozak consensus sequence

<220>

<221> misc_feature

<222> (1)..(1)

<223> n is g or a

<220>

<221> misc_feature

<222> (2)..(3)

<223> n is a, c, g, or t

<400> 159

nnnatgg

7

<210> 160

<211> 17

<212> DNA

<213> Artificial

<220>

<223> Proposed Reverse PCR primer sequence

<400> 160

tgagctgctg ccacaaa

17

<210> 161

<211> 7

<212> DNA
<213> Artificial

<220>
<223> Seven base pair inverted repeat region

<400> 161
caacttt

7

<210> 162
<211> 7
<212> DNA
<213> Artificial

<220>
<223> Seven base pair inverted repeat region

<400> 162
aaagttg

7

<210> 163
<211> 4
<212> DNA
<213> Artificial

<220>
<223> PCR forward primer addition

<400> 163
cacc

4

<210> 164
<211> 4
<212> DNA
<213> Artificial

<220>
<223> Overhang in cloning vector

<400> 164
gtgg

4

<210> 165
<211> 7
<212> PRT
<213> Artificial

<220>
<223> C-terminal polyhistidine tag and free carboxyl group

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Xaa = free carboxyl group

<400> 165

His His His His His His Xaa
1 5